

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACCGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCCTCTTCCCG
CAGCGCTACCCGCCATCGCCTGCCGCCGGCCGCTGGGGCTCCTGCCGCTTCTGCTG
CTGCTGCCGCCGCCGGAGGCCAAGAAGCCGACGCCCTGCCACCAGTGCCGGGGCT
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAAGAACTTGGCGGGGGAAACA
CGGCTTGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGTGTCTGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGGAGATGGAGCAGACA
GGGCGACGGGTCTGCCGGTGCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCCAGTGAGTGTGAAGTGGCTGGTGCT
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG
GGCTGCACAGGGAAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCAGGGAGCA
CGGACAGTGTGCAAGATGTGGACGAGTGTCACTAGCAGAAAAAAACCTGTGTGAGGAAAAACG
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGCTGACGGCTCGAAGAAACG
GAAGATGCCGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTACCCCTAAATTATTAGAAGGATGTCC
CGTGGAAAATGTGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGGGGAGAGGCTGC
CTGCTCTCTAACGGTGATTCTCATTGTCCCTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTTGTATATTTGATACAGTTCTTGTAATAAAATTGACCATTGTAGGTAAATCAGG
AGGAAAAAAAGGGCGCCGCGACTCTAGAGTCGACCTGCAGAAC
TTGCCGCCATGCCCAACTGTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTCAAAATAAGCATTTCACTGCATTCTAGTTGTGGTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGAATTAATTGCCGCAGCACCATGCCGTAAAT
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGCGAAAGAACCGACTGTGGAATG
TGTGTCAGTTAGGGTGTGAAAGTCCCCAGGCTCCAGCAGGAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLPLLLLLPAPPEAAKKPTPCHRCGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNEHTSICTACDESCKTCGTLNRDCGECEVGWLDE
GACVDVDECAAEP PCSAAQFCKNANGSYTCECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAAC TGCACCTCGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACCGTCCGCCAGGCCGGAGGCACGCCAGCCGTCTAAACGGGAACAA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGGCCAGGTGCGTAGGTGCG
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGCAGCATGCCCGGAGGAGCGCCTTC
CCTGCCGCCGCGCTCTGGCTCTGGACATCCTCTGTGCCCTGCTGGCACTGCAGGGCGGAGGC
CGGGCCGCCGAGGAGAGCCTGTACCTATGGATCGATGCTACCAGGCAAGAGTACTCA
TAGGATTGAAGAAGATATCCTGATTGTTCAGAGGGAAAATGGCACCTTACACATGAT
TTCAGAAAAGCGCAACAGAGAAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC
CTGGCAAGCTGCAGGGCAGGCAGAAACTTCTATGAATTCTGTCCTGCGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGAACAGTGCCTCACAGGCA
TCAGTTGTTCAAGTTGGTTCCCATGTTGGAAAACAGGATGGGTGGCAGCATTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCT
TCTTAAACATGTCAACAAGCTGAGTGCCTCAGGGTCCACGGACCTCACTGTGAGAAAGCCCTTG
GAAAGACGCATCTGCGAGTGTCTGATGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCACGATGTATGAATGGTGGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAAC TGTGACAAAGCAAAC TGTCAACCACCTGCTTAAATGGAGGGACC
TGTTCTACCCCTGGAAAATGTATTGCCCCCTCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACACCCCTGTCGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT
CCAAAGGTTACCAAGGGAGACCTCTGTTCAAAGCCTGTGCGAGCCTGGCTGGCACAT
GGAACCTGCCATGAACCCAAACAAATGCCAATGTCAGAAGGTTGGCATGGAAGACACTGCAA
TAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGCGCCAGCTCAGGCAGC
ACACGCCCTCACTAAAAAGGCCAGGGAGCGGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTACAGCTTGTAAACCTTCA
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAAATACTGGCCTGAATTTCATTAGCT
TCATTATAAACTCACTGAGCTGATATTACTCTTCTTTAAGTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTCTTCTGTTCACTGCTGGACAGATTATATTATGTCATTGAA
TCAGGTTAAATTTCACTGAGCTGAGTGGCAGATATTCTAAACATGCAATTGATTGGT
GTCTGGGGCAGGGAAACATCAGAAAGGTTAAATTGGGCAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTCTAGATTATTGTCAGATATTAGAT
GTTTGTACATTAAAATTGCTCTTAATTCTAAACTCTCAATACAATATATTGACCT
TTACCAATTATTCCAGAGATTCACTGATTAAAAAAATTACACTGTGGTAGTGGCATT
AAACAAATATAATATTCTAAACACAATGAAATAGGGAAATATAATTGATGAACTTTGCAT
TGGCTTGAAGCAATATAATATTGTAACAAAACACAGCTCTAACCTAACAAACATT
ACTGTTGTATGTATAAAATAAGGTGCTGTTAGTTTTGGAAAAA
AAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCGAGAGCTTGGC
CGCCATGGCCCAACTGTTTATTGCAAGCTTATAATG

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKICPPGLEGEQCEISKCPQPCRNGGKCIKGSKCKCSKGYQGDLCSPKVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGCGTCCGGCGTCGAGAGCCAGGAGGCAGGAGGCCAGCCTGGG
CCCCAGCCCACACCTTCACCAGGGCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCGTGGCGCCGG
GAGCTAGCACCAGGGTCTGCACCTGCAGGGCATCCGGACGCGGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGCCGTGCCAGCAGACTGTGCCCTGCCACTCTGGCGCCATCT
GTTACTGTGACCTCTCTGCAACCGCACGGTCTCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGCGTGCCACCCCTTCCCCGATCCAAGGATGTATGCATGGAGGTGTATCTA
TCCAGTCTTGGAACGTACTGGACAACGTAACTGTAACCAGTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTCTGGGCATGACCCTGAGGGCATTCGTACCGCCTGGCACCA
TCCGCCATCTCCTCGTCATGAACATGCATGAAATTATAACAGTGTGAACCCAGGGGAG
GTGCTTCCCACAGCCTTCGAGGCCTCTGAGAACGTGGCCAACCTGATTGATGAGCCTCTTGA
CCAAGGCAACTGTGCAGGCTCTGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCGTCCGTGCCCCAGAACCTGCTGTCTTGAC
ACCCACCAGCAGCAGGGCTGCCCGGGTGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCG
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCC
CACTGCCAACAGCTATGTTAAATAACATGACATCTACAGGTCACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAACATGGCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTCCTATAACAGGGAGGCATCTACAGCCACAGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTAAATACTGGACTGCCAACCTCTGGGCC
CAGCCTGGGCGAGAGGGCCACTTCCGCATCGCGCGCGTCAATGAGTGCACATCGAG
AGCTTCTGTCTGGGCGTCTGGGCGCGTGGGCATGGAGGACATGGTCATCACTGAGGCTG
CGGGCACACCGCGGGGTCCGGCCTGGGATCCAGGCTAACGGCCGGGAAGAGGCCCAATG
GGCGGTGACCCAGCCTCGCCGACAGAGCCGGCGCAGGGGGCGCCAGGGCGCTAAT
CCCAGCGGGTCCGCTGACGCAGGCCCGCTGGGAGGCCGGCAGGCAGACTGGCG
GAGCCCCAGACCTCCAGTGGGACGGGGCAGGGCTGGCAGGGAAAGAGCACAGCTGCAG
ATCCCAGGCCTCTGGCGCCCCACTCAAGACTACCAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCGTATTCTTTTTTTTTAGACAGGGTCTTGCTCCG
TTGCCCAAGGTGGAGTGCAGTGGCCATCAGGGCTCACTGTAACCTCCGACTCCTGGTTCA
AGTACCCCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCAACACCTGGC
TAATTTTGATTTTGTAAGAGGGGGTCTCACTGTTGCCAGGCTGGTTTCGAACCT
CCTGGCTCAAGCGGTCCACCTGCCTCCGCTCCAAAGTGTGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTTCACTGTTTAAAAA
TAAAACCAAAAGTATTGATAAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCGRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQRLLGHDPG
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N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCTGGCCCTTTCACAGCAAGCTTNTGCNATCCGATTGTTGTCTCAAATCCA
ATTCTCTGGGACACATNACGCCTGTCCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGGCAAGCGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTGGG
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

100 200 300 400 500 600 700 800 900 1000

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTGGCCCTGCAGCCAGGCAGTGCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCATGGGAGCCTGTCCTGGTTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCCCTGACCCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCCTTAACCCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA
GGGCCAGGCCTCACATTGTTGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSDT
DPPADGPSNPLCCCFFHGPAGFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCACCGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCGCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGCCAGATCCCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTCAGGTCAACGGCGTGCATCTCCGCCACGCCAGGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGAAGAGCAAAGACTG
CGTGGTCACGGAGATCGTGGAGAACAACTATAACGCCCTCCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCCAGGGCGCCGCCAGGCTTCCGCAGGCCAGAAC
CAGCGCGAGGCCACTTCATCAAGGCCCTTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAACAGAAGCAGTCAGTTGAGTTGTGGCTCCGCCACCCGCCAGAACCGCACAC
GGCGGCCCTCAGCCCTCACGTAGTCTGGGAGGCAGGGGCAGCAGCCCTGGCCCTCCC
CACCCCTTCCCTTAATCCAAGGACTGGGCTGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCCTGAGGCCCGAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGT
CCCCAGGGCGGCTGGCACAGTGCCCTCCGGACGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTCAACCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCCTGAAGCC
CGCTGAAAGGTCAAGCGACTGAAGGCCTTGCAGACAACCGTCTGGAGGTGGCTGTCCCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGAAACTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTGTTCAAGGAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCCCACCCCCACTCCAGCCC
CGGAATAAAACCATTTCCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDCVFTEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTCATGGAG
GACAGCAGCAAAGAGGGCAACACAGGGTGTAAAGACCAAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
CATTGATTTGCTGTTATTTTTCTTTCTTTCCCACCAATTGTATTTAT
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGCTTTCT
GAAGTCTGGCTTATCATTCCCTGGGCTCTACTCACAGGTGTCAAACCTCTGGCCTGCC
CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCCAGGGCGTAACCGTACTCTACCTCCACAACAAACAAATTAAATAATGC
TGGATTCCTGCAGAACTGCACAATGTACAGTCGGTGACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCAAGAAATGTCAGAGTCTCCATTGCAAGGAAAC
AATATTGACACCATTACAGGGCTGCTTGCCCCAGCTTGAAAGCTTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCCTCCGGGAGGGTATTAGCC
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAATCGAATTGCTGTATATCCGACATGGCCTCCAGAA
TCTCACGAGCTGGAGCGTCTATTGTTGACGGGAAACCTCTGACCAACAAAGGTATGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATGTCAGGCTCTATTGCAAGGACAACAGAT
CACCCCTCCTCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACAGAT
AAACACATTCCCTTGACAGCCTCTCAAATCTGCGTAAGCTGAAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGTTTGATAATCTCCAAACCTGAAGCAGCTC
ACTGCTCGGAATAACCCCTGGTTTGACTGCACTTAAATGGGTACAGAATGGCTCAA
ATATATCCCTCATCTCAACGTGCGGGTTCATGTCACAGGCTCTGAACAAAGTCCGGG
GGATGGCGTCAGGGAATTAAATATGAATCTTGTCCCTGCCCACACGACCCCCGGCCTG
CCTCTCTCACCCAGCCCCAAGTACAGCTCTCCGACCAACTCAGCCTCCACCCCTCTAT
TCCAAACCCTAGCAGAAGCTACACGCCCTCAACTCCTACACATCGAAACTCCCACGATT
CTGACTGGGATGGCAGAGAAAGAGTGAACCCACCTATTCTGAACGGATCCAGCTCTATC
CATTGTAATGATACTCCATTCAAGTCAGCTGGCTCTCTCTTACCGTATGGCATA
CAAACACATGGGTGAAATGGGCCACAGTTAGTAGGGGGCATCGTTCAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
TGTTAGTGCCACTGGATGTTTAACCTACCGCGCGGTAGAAGACACCAATTGTTCAGAGGC
CACCAACCATGCCCTCATCTGAACAAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGATGGGGCGCGGTGATATT
GTGCTGGTGGTCTTGCTCAGCGTCTTGCTGGCATATGCACAAAAGGGCGCTACACCTC
CCAGAAGTGGAAATACAACCGGGCCGGAAAGATGATTATTCAGATCGTCTCTAAATAACGAT
AGGACAACCTCCATCTGGAGATGACAGAAACCAAGTTTCAAGTGTCTCTAAATAACGAT
CAACTCCTAAAGGAGATTCAAGACTGCAGCCATTACACCCAAATGGGGCATTAAATTA
CACAGACTGCCATATCCCCAACAAACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGCGGACAATTAGACTCTTGAGAA
CACACTCGTGTGTCACATAAGACACGCAGATTACATTGATAAAATGTTACACAGATGCAT
TTGTCATTGAAACTCTGTAATTATACTGGTACTATATAATGGGATTTAAAAAAAGTG
CTATCTTCTATTCAAGTTAAATTACAAACAGTTGTAACCTTTGCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGaffLKSwlIISLGLySQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTvLYLHNNQINNAGFPaELHNVQSVHTVLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKEELHLDNsISTVGVEDGAFREAIaLKLFLSKNHLSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLNSNLQLTARN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMARVELNMNLLSCPTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTSKLPTIPDWDGRERVTppISeRIQLSIHFVND
TSIQVSWLSLFTVMAyKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGTKKDnsILEMTETSFQIVSLNNdQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGCGGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGCTCCGTCCGCCTCCACGAGCG
ATCCCCGAGGAGAGCCGGCCCTCGGCAGGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTCGGCCCTGCC
TCGCTTCCCAGGCAGGGCTGCAGCCTTGCCCTTGCCTGCAAGGAAATGGAAAAGATGCTCGCAGGCT
GCTTTCTGCTGATCCTCGGACAGATCGTCTCCCTGCCAGGGCAGGGCAGGGAGCAGGTCACTGTGGAGGTCCATCT
CTAGGGGAGACACGGCTGGACCCACCGCAGACGGCCCTCTGGAGAGTCTGTGAGAACAAGCGGGCAGACC
TGGTTTCATCATTGACAGCTCCGAGTGTCAACACCCATGACTATGCCAAAGGTCAAGGGAGTTCATCGTGGACA
TCTTGCAATTCTTGACATTGGTCTGTGACCCAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGAATG
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCGTGTCAAGAGGATGCGGCATCTGTCCACGG
GCACCATGACTGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCGGCCCTG
GGGAGAATGTGCCACGGGTATAATGATCGTACAGATGGAGACTCAGGACTCCGTGGCGAGGTGGCTGCTA
AGGCACGGGACACGGGCATCTAATCTTGCCATTGGTGTGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG
GGAGTGAGCCCCATGAGGACCATGTCCTCTGTGGCAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTCC
AGAAGAAGTTGTGCCACGGCCACATGTGCAGCACCCCTGGAGCATAACTGTGCCACTCTGCATCAACATCCCTG
GCTCATACGTCTGCAGGTCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCGAGAATCCAGGATCTGT
GTGCCATGGAGGACCACAACGTGAGCAGCTGTGTGAATGTGCCGGCTCTCGTGTCCAGTGTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGCTGTGGACTACTGTGCCCTAGAAAACCACGGATGTGAAC
ATGAGTGTGTAATGCTGATGGCTCTACCTTGCCAGTGCATGAAGGATTGCTCTTAACCCAGATGAAAAAA
CGTGACAAGGATCAACTACTGTGACTGAACAAACCGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGAAAACCTGCAGCCAGTGGACCACTGTGCAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTGAACACCGGAGGATTCTCGTGTCCAGTGTCAAGAGGCTTC
TCATCAACGAGGACCTCAAGACCTGCTCCGGTGGATTACTGCCCTGCTGAGTGACCATGGTTGTGAATACTCCT
GTGTCACATGGACAGATCTTGCTGTCACTGTGCTGAGGGACACGTGCTCCGCAGCGATGGGAAGACGTGTG
CAAATGGACTCTTGCTCTGGGGACACGGTTGTGAACATTGCTGTGAAGCAGTGAAGATTGTTGTG
GCCAGTGTGTTGAAGGTTATAGTACTCCGTGAAGATGGAAAACCTGCAAGAAGGAAAGATGTCTGCCAAGCTATAG
ACCATGGCTGTGAACACATTGCTGTGAACAGTGACGACTCATACACGTGCGAGTGCTTGGAGGGATTCCGGCTCG
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAATCAACCCACCATGGTGGCAACACATTGTTGTTA
ATAATGGGAACTCTACATCTGCAAATGCTCAGAGGGATTGTTCTAGCTGAGGACGGAAAGACGGTCAAGAAAT
GCACTGAAGGCCAATTGACCTGGCTTGTGATCGATGGATCCAAGAGTCTGGAGAAAGAGAATTGGAGGTG
TGAAGCAGTTGTCATGGAATTATAGATTCTTGACAAATTCCCCCAAAGCCGCTCGAGTGCGTGTCCAGT
ATTCCACACAGGTCCACACAGGTTCACTCTGAGAAACTTCAACTCAGCAAAGACATGAAAAAGCCGTGGCC
ACATGAAATACATGGAAAGGGCTATGACTGGCTGCCCTGAAACACATGTTGAGAGAAGTTTACCCAAG
GAGAAGGGGCCAGGCCCTTCCACAAGGGTGCCAGAGCAGCCATTGTTGTCACCGACGGACGGCTCAGGATG
ACGTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTACACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG
AGGAGGAACATACAAGAGATTGCCCTGAGCCCACAAACAAGCATCTTCTATGCCGAAGACTTCAGCACAATGG
ATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGAACTGCCAAAACGGTCCAACAGCCAACAGAAATCTGAGCCAGTCACCATATAATATCCAAGACCTACTTT
CCTGTTCTAATTTGCACTGCAACACAGATATCTGTTGAAGAAGACAATCTTACGGTCTACACAAAGCTTT
CCCATTCAACAAAACCTCAGGAAGCCCTTGGAGAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT
TCCAGAACCTGCAAACGAAGAAGTAAGAAAATTAAACACAGCGCTTAGAAGAAATGACACAGAGAAATGGAAGGCC
TGGAAAATGCCCTGAGATACAGATGAAGATTAGAATCGCAGACATTTGTTAGTCATTGTATCACGGATTACAAT
GAACCGCAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGAGTAAACAAATCAGTACTGA
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTACACTAACTGTATAAATTATCTAGGAAAAAAATCCT
TCAGAATTCTAAGATGAATTACCGAGTGAAGATGAATAAGCTATGCAAGGTATTGTTAATATACTGTGGACAC
AACTGCTCTGCCCTCATCTGCCCTAGTGTGCAATCTCATTGACTACGATAAAAGTTGCACAGTCTTACTT
CTGAGAACACTGCCATAGGAAATGCTTTTTGTACTGGACTTACCTGATATGTATATGGATGTATG
CATAAAATCATAGGACATATGTAATTGTGGAACAAGTGGATTTTTATAACATATTAAACCACTTCAG

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRHARTHPOQTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFRKSEVERAV
KMRHLSTGTMGLAIQYALNIAFSEAE GARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIQVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKG
EHECVNMEESYYCRCHRGYTLDPNGKTCRSVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSRGKTCAKLDSCALGDHGCE
HSCVSSEDFVCQCFCFGYILREDGKTCRRKDVCQAIHDGCEHICVNSDDSYTCECLEGFR
LAEDGKRCRCKDVCKSTHGCEHICVNNNGNSYICKCSEGFLAEDGRRCKCTEGPIDLVF
GSKSLGEENFEVVVKQFVTGIIDS LTISPKAARVGLLQYSTQVHETFLRNFNSAKDMK
HMKYMGKGSMTGLALKHM FERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWAS
GITMYAVGVGKAIEEELQEIASEPTNKHLFYAEDFSTMDEI
SEK LKKGICEALEDSDGRQDS
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCGTCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCGTACTCCGTCCCGCCAGGGAGGGC
CATGATTCCTCCCTCCCGGGCCCGTGGTACCAACTTGCTGCGGTTTTGTTCTGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTGTCCAGCGTGGTACACCTGCACGGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCCTGCGCTGGAGGGCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGCCACAGCATAAAACCT
TAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTCCAGACTTCTTGACCCAGCATTAGATGTCATCCGTG
GGTCTTAAGCCTACCAACCTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTTGAGCTGGTACCCCTGGTGGACTGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCACCGCCGGGCAAGGCCCTGGAGGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCCTGCCCTGGCCAAGAGACTCAGACACAATCTCAAAGAATGGACCC
TTCCTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCATGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAGACTGGCTCTGGTAT**GATGAC**
CCCACCACTATTGGCTAAAGGATTGGGCTCTCCTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTC
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTCCAGTCAGTGAGTCTCCAGGC
CCCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCGT
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGCAGAGGATAGGAAATCTC
TTATTAAAACATGAAATATGTGTTGTTCTATTGCAAATTAAATAAGATAACATAA
TGTTGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTACQCNVTLEVSTGPGAA
VVAGAVVGTIVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCA**ATGAAACGCCTCCGCTCTAGGGTTTCCACTTG**
TTGAATTGTCCTATACTCAAAATTGCAACAGACACCTTGTCTCCAAATGAAAATGTGA
AATACGCAATGGAATTGAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGAAATTAACTCAGTCCTGTGGCAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTGTATGTGTACCTGGCTCAGATCCAGCAGTAACCA
AGACAGGTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGCCATT
TAGATAATGTCTGTATAGCTGCAAATATTAAATAAAAATTAAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAAACA
CTATCTCAGCCAAGGACACCCCTTCTAACTCAACTCTTAAGGTTACAAGAACAAACA
AATTTGTTCAAAGGGATACATTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACACTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTGAT
TCATATAACATGAAACATATTCACTCCTCATATGAATATGGATGGAGACTACATAAATATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGAGTTGCATTTCATTTATATTATA
AGAGTATTGGCCTTGTCTTCATCATCTGACAACCTCTTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATATGAACATTGAAAAAAATAACATTACATTAAAGTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGTGCATTGGATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTGCAATTGATGTCCTCTGGTCCTTCATTGGTATTAAAGATTATAATATTC
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGCTTGCCATATGCATTTC
ACCTTCTGGTTCTTCAGTGAATTCAAAGCACCAGGACAACAATTCAAAAAATCTTGCTG
TAGCCTATTCTTGCTGAATTGTTCTTGTTGGATCAATACAAATACTAATAAGCTCT
TCTGTTCAATCATTGCCGACTGCTACACTACTTCTTAGCTGCTTGCATGGATGTGC
ATTGAAGGCATACATCTATCTCATTGTTGGGTGTCATCTACAACAAGGGATTGGCA
CAAGAATTTTATATCTTGCTATCTAACCCAGCCGTGGTAGTTGGATTTCGGCAGCAC
TAGGATACAGATATTATGGCACAACCAAGTATGTTGGCTTAGCACCGAAAACAACCTTATT
TGGAGTTTATAGGACCAGCATGCCATAATCATTCTGTTAATCTCTTGCTTGGAGTCAT
CATATAACAAAGTTTCGTACACTGCAGGGTTGAAACCAGAAGTTAGTGCTTGAGAAC
TAAGGTCTGTGCAAGAGGAGGCCCTCGCTTTCTGTTCTCGGCACCACCTGGATCTT
GGGGTTCTCCATGTTGTGCACGCATCAGGTTACAGCTTACCTCTCACAGTCAGCAATGC
TTCCAGGGATGTTCATTTTATTCTGTGTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTTCAAAATGCCCCGTTGGATGTTAAGGTAACATAGAGAAC
GTGGATAATTACAACACTGCACAAAAATAAAATTCCAAGCTGTGGATGACCAATGTATAAAA
TGACTCATCAAATTATCCAATTATTAACACTAGACAAAAAGTATTAAATCAGTTTCT
GTTTATGCTATAGGAACGTGAGATAATAAGGAAAATTATGTATCATATAGATATACTATGT
TTTCTATGTGAAATAGTCTGTCAAAATAGTATTGCAAGATAATTGGAAAGTAATTGGTT
CTCAGGAGTGTATCACTGCACCCAGGAAAGATTCTTCTAACACGAGAAGTATATGAA
TGTCTGAAGGAAACCACTGGCTGATATTCTGTGACTCGTGTGCTTGAACACTAGTCC
CCTACCACTCGGTAATGAGCTCCATTACAGAAAGTGAACATAAGAGAACATGAAGGGGCAGA
ATATCAAACAGTGAAGGAAATGATAAGATGTATTGAAATGAACTGTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAAGAATTGAAGAACACATTACCACTTGTGAA
TTGTTCTGAACCTAAATGTCCACTAAAACAACCTAGACTCTGTGCTAAATCTGTTCT
TTCTAATATTCTAAAAAAAGGTTACCTCCACAAATTGAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEYVRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL
SNSTLTFVKTVNNFVQRDTFVVWDKLSVNHRRTLTKLMHTVEQATLRIQSFKTTEFDT
NSTDIALKVFFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSGNVAVAFLYYKSIGPLLS
SSDNFLLPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF
WNYS PDTMNGSWSSEGCELTYSNETHTSCRCNLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAI CIFTFWFSEI QSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFC SIIAGL
LHYFFLAFAFWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAA LGYRYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVVLHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKI QEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTGCATTTATATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTTACCTTC
TGGTTCTCAGTGAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCTCCTCCCAGATCCGAACGGCCTGGGCGGGTCAACCCGGCTGGGA
CAAGAAGCCGCCGCTGCCTGCCCAGGGCCGGGAGGGGGCTGGGCTGGGCGGGAGGC
GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGTGCAATCCGATAAGAAATGCTCGGG
TGTCTTGGGCACCTACCGTGGGCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG
CCGCCGCCGCGTCAGAGCAGGAGCGCTCGTCCAGGATCTAGGGCACGACCATCCAACCC
GGCACTCACAGCCCCGAGCGCATCCCGTCGCCGCCAGCCTCCGCACCCCCATGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGGGTGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCGTGGCCGGCGCCCCCTGCCCTCTCGGACGCCGGGCC
CCACGTGCACTACGGCTGGCGACCCCATCCGCCTGCCACCTGTACACCTCCGGCCCC
ACGGGCTCTCCAGCTGCTTCTGCCATCCGTGCCACGGCGTGGACTGCCGCCGGG
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGCCACCGTGGCATCAAGGG
CGTGCACAGCGTGCAGGTACCTCTGCATGGCGCCACGGCAAGATGCAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAACGCCCTCCGGTCTCCCTGAGCAGTCCAAACAGCGGAGCTGTACAAGAA
CAGAGGCTTCTTCACTCTCATTCCGCCTGCCCCATGGTCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTGGCTTGTACCGGACTGGAGGCCGTGAGGAGTCCAGCTTGAGAAGTAA
GAGACCATGCCGGCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGACG
TGCTTCTACAAGAACAGTCCTGAGTCACGTTCTGTTAGCTTAGGAAGAAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCACGTTCTAGCCAATAGACTGTCTGAT
CATAACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGCCCCCATTCTGCTCCCTCGA
GGTGCTGGACAAGCTGCTGCACTGCTCAGTTCTGCTGAATAACCTCCATCGATGGGAAC
TCACTCCTTGGAAAAATTCTTATGTCAAGCTGAATTCTCTAATTTCAGGAACAGGTGATCCACTCTGTA
CCCAGGAGCAGCCAGAACAGCAGGAGTAGTTAATTCAAGGAAACAGGTGATCCACTCTGTA
AAACAGCAGGTAATTCACTCAACCCATGTGGAATTGATCTATCTACTTCCAGGG
ACCATTGCCCTCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCATGGCCACCAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGGCCCTGGGACAACCTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCTGAGAATAACTGCTGTCCTGGTGTACCTGC
TTCCCATCTCCAGGCCACCAGCCCTGCCACCTCACATGCCCTCCCATGGATTGGGGCCT
CCCAGGCCCCCACCCTTATGTCAACCTGCACTCTGTTCAAAATCAGGAAAGAAAAGAT
TTGAAGACCCCAAGTCTGTCATAACTTGTGCTGTGGAAGCAGCGGGGAAGACCTAGAAC
CCTTCCCCAGCACTTGGTTCCAACATGATATTATGAGTAATTATTTGATATGTACA
TCTCTTATTTCATTACATTATTATGCCCAAATTATATTATGTATGTAAAGTGAGGTTG
TTTGTATATTAAAGGAGTTGTTGT

FIGURE 22

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLQYSEEDCAFEE
EIRPDGYNVYRSEKHLRPLVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSDMPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCTGCCTCGCTCCGCCGGGACCCCTGACCTCCTCA
GAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTGCTG
CTGCTGCCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCAA
AGAAGACTGTTCTCCAGATTAGAGTGGAAAGAAACTGGTCGGAGTGTCTCCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAATGTGACAAGAAGTGTGATGCCGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG
AGCAAGGCCAAACCTGGAAGAGGATACAGTCAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTTTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAAATCCAGCTCTGAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAA
ATCCCAGACTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAAACTGGAAC
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAAATATTCTGTGAAGCCCGCAATT
TGTTGGATATCGCAGGTGTCCCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCGTAGTAGTTGTGGCCTAGTGATTTCCGTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTTCATCTAA
AGCCACGACAATGAGTGAATGTGCAGTGGCTCACGCCCTGTAATCCAGCACTTGGAAAGG
CCGGGGCGGGCGGATCACGAGGTCAAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAAATCACTGAACCCGGGAGGCGGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAAAATA
AATAAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

FIGURE 24

MARRSRHRLLLLLLRLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKTVSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNL
EEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD
GIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN
SVGYRRCPGKRMQVDDLNISGIAAVVVVA
LVI
SVCGLGV
CYAQRK
GYFSK
ETSFQ
KSNSSS
KATTM
SENVQ
WLTPV
I PALW
KAAAGG
SRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGGCAACATTTATTAACATGCTCCACAGCCCGGACCTGGCAT
CATGCTGCTATTCCCTGCAAATACTGAAGAAGCATGGATTAAATATTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTACATACATCCACCTTCAAAAAGTACATCAATA
TTATATCATTAAGGAAATAGTAACCTCTCTTCTCAAATATGCATGACATTGGACAATG
CAATTGTGGCACTGGCACTTATTCAGTGAAGAAAAACTTGTGGTTCTATGGCATTATCA
TTTGACAAATGCAAGCATCTCCTTATCAATCAGCTCTATTGAACTTACTAGCACTGACTG
TGGAACTCTTAAGGGCCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCTATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTTCCCAGCCAGATTGCC
AGCTAACACACAGATTCTCTCCTACAGACTAACAAATATTGCAAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTATCTCAGTCACCAAT
ATTAATGTAAGGAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTTACTGA
ACTGCCTGAAAATGTCGACTGAGCAACTTACAAGAACTCTATATTAAATCACAAC
TGCTTCTACAATTCACCTGGAGCCTTATTGGCTACATAATCTTCTCGACTTCATCTC
AATTCAAATAGATTGCGAGATGATCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT
TCTGATGATTGGGAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAGCCTCTTATCA
ATCTTCGCAGCCTGGTTAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCCTGGTT
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCCATGT
TGCTCTTCAAAAGTTGTAATCTCAAATTGGATCTAAATAAAACTCTATTAAATAGAA
TACGAAGGGGTGATTAGCAATATGCTACACTTAAAGAGTTGGGATAAAATAATATGCCT
GAGCTGATTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTAAAGAAAATAGAAGC
TACTAACAAACCTAGATTGCTCTACATTCAACCCAAATGCATTTCAGACTCCCAAGCTGG
AATCACTCATGCTAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCTGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCATCAGGTGTGACTGTGTCATCCGTTG
GATGAACATGAACAAAACACATTGATTGAGGCCAGATTCACTGTTTGCCTGGACC
CACCTGAATTCCAAGGTCAAATGTTGGCAAGTGCATTTCAGGGACATGATGGAAATTGTT
CTCCCTTCTTATAGCTCTGAGAGCTTCTCTAATCTAAATGTTAGAAGCTGGGAGCTATGT
TTCCTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTG
GTCAAAAACCTTGCCTAATACCCCTGACAGACAAGTTCTATGTCCTATTGAGGGAAACACTA
GATATAATGGCGTAACCTCCAAAGAAGGGGTTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAAATG
GCTCTTGAATATTAAAATAAGAGATATTGAGCCATTCAAGTTGGTGTCTGGAAAGCA
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA
TGCTGCGCAAAGTGCCTGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTATCAGAAAAACAGAAAAAAA
TGTGTAATGTCACCACCAAGGTTGCACCCCTGATCAAAAAGAGTATGAAAAGAATAATAC
CACAAACACTTATGGCCTGTCTGGAGGCCCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCCAGAAATGAACACTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGATAAAATCTCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTATAGGTTACCAACAAATATGTCCT
AAAAACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNIAKIEYSTDFTPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLRLHLNSNRQLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRLSIVAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVNLKFLLDNKNPINRIRRGDFSNMLHLKELGINNMPPELISIDSIAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNVQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRTAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMNCGGHSYVRNYLQKPTFALGELYPP LIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCTGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGTGGAGTAGATGAGGAATGGCTCGTATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCGTTCCCTCCATGTGTCTCCTACAAAGTTGTTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTGTCTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAATGCCTCAATAACCTGAAGGCCAGGCCAGAATTGCCAACAAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTGGCTGGTCACTATGGTGTACTCATATGTGGTATTATGTGAGGCAAAATCAGGAG
GATGCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTATTGAGAAAGAAAGAAA
GTAGTTGCGATTGCAGTAGAAATAAGTGGTTACTTCTCCATCCATTGTAAACATTGAA
ACTTTGTATTCAGTTTTTGAAATTATGCCACTGCTGAACTTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTTT
AATTAAAAGCAAATAAAAGCTTAACTTGAACCAGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMC PKGCLCSSGGLNVTCSNANLKEIPRDL
PPE TVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLDR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPF
LNAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGGG
GGCGTGAGGAGCATGCCAGCCCCCTGCTGGCAGCCCATCCTCCTGCTGGTGC
GGGCTCAGTGTGTCAGGCTCGGCCACGGCTGCCGCCCCGCTGCGAGTGCTCCGCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGTCTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCGTGGAGGCCGG
CCTTCAACAAACCTCTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCAGAACAAAGAT
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCACCAGCGCCTCAGGGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCGCTGTCCCACCTGCACGGCCT
CATCGTCCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCCTACTTGGACACCATGACACCCAAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCCCTCAACCTCTCCTACAACCCCCATCA
GCACCAATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGGCAGCTGGCCGTGGAGCCCTATGCCCTCCGCCCTCAACTACCTGCGCGTGTCA
TGTCTCTGGCAACCAGCTGACCAACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTCGGCTCCTGTGGGTGTC
CGCCGCTGGCGGCTCAACTCAACCGGAGCAGGCCACGTGCGCCACGCCAGTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTTCACCTGCCGCC
CCCGCATCCGGGACCGAAGGCCAGCAGGTGTTGTGGACGAGGGCCACACGGTGCAGTT
GTGTGCCGGGCCGATGGCGACCCGCCGCCCCCATCCTCTGGCTCTCACCCCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCCGGCAACGAC
TCCATGCCGCCACCTGCATGTGCGCAGCTACTGCCACTGGCCCCATGCCAACAA
GACCTCGCTTCATCTCCAACCAGCCGGCGAGGGAGAGGCCAACAGCACCGCGCCACTG
TGCCTTCCCTCGACATCAAGACCTCATCGCCACCCATGGGCTTCATCTCTTCC
CTGGCGCTGTCCTCTGCCCTGGTGTGCTGTTCTGGAGGCCGGCAAGGGCAACAC
AAAGCACAACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGCATCAGCTCCGCC
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCCGGGGCGGGGGCAGGGACCCCCGG
GGCGGGCGGGCAGGGGAAGGGGCTGGTGCACCTGCTCACTCTCAGTCTTCCACCTC
CTCCCTACCCCTCTACACACGTTCTTCTCCCTCCGCCCTCCGTCCTGCTGCC
CCAGCCCTCACCACCTGCCCTCTTCAACCAGGACCTCAGAAGGCCAGACCTGGGACCCCC
CCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACAGCGGCAGAGTC
ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACCTGGGTTCAATAATTATGGATTT
TATGAAAACCTGAAATAATAAAAAAGAGAAAAAAACTAAAAAAAAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL
GLRSNRLKLIPLGVFTGLSNLTQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSIHCNLTAAPYLAVERHLVYLRFNLNSYNPISTIEGSMLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTLEESVFHSVGNLETLILDSNPLA
CDCRLLWVFRWRRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVFPDGTLEVRYAQVQDNGTYL
CIAANAGGNDNSMPAHLHRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCACACGGTCCGCACCTCGCCCCGGCTCCGAAGCGGCTGGGGGCCCTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTCCTGC
TGTCGCCTGCTGCTGGCGCCGGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGCACCGTGGTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTACTTGGGAGAAGA
GAGCCCTCGAGATAATCGAATTCACTGGTACCTCACGCCAACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACCCATCATCACTGGTT
ATAAAATCTTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTTCTGGGAGCAAG
CCTGCAGCCGGCTCACCTGGAGAAAGGTGACCAAGAAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAACGCTGTTGCTACACTGTGAGGGTCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTCCCTTCCCTCAACAAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCGGTGCCT
CCTCCTCCAGCACCTACCAACGCCATCATCGTGGGATCGTGGCTTCATTGTCTCCTGCTG
CTCATCATGCTCATCTCCTGGCCACTACTTGATCCGGACAAAGAACCTACCTGACACA
TGAGGCAGGCTCCGACGATGCTCCAGACGGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGACGACAAGAAGGAATATTCACTTAGAGGCGCTGCCACTTCTGC
GCCCCCCAGGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCCGCTGCTCCCCAGCCCACCCACCCCTGTACAGAAATGTCTGC
TTTGGGTGGGTTTGTACTCGGTTGGAATGGGAGGGAGGAGGGCGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA
AACAAAAAACAA

FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRQLVTSTPHELYSISISNVALADEGEYTCSIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTCTTCTCCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTGAAATTGTGCTGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAATGCTGCTTGGATTCTGTT
GCTGGAGACGTCTTTGCCGCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTTACCAATTATTCTGCATGGCAATT
CCTCACTCGACTTTCCCTAATGAGTCGCTAACCTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTTCTGGGGCTGCAGCTGGTAAAAGG
CTGCACATCAACAACAAGATCAAGTCTTCGAAAGCAGACTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAAGACCCGGGGCTTCCAGG
ACTTGAACAAAGCTGGAGGTGCTCATTAAATGACAATCTCATCAGCACCCACTGCCAAC
GTGTTCCAGTATGTGCCCATACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCTGCTAGAGGATAACCC
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGTCCTTGAAAAACCGAGTGGATTCTAGTCTCCGGCCCGCTG
CCCAAGAACAGACCTTGCTCCTGGACCCCTGCCACTCCTTCAAGACAAATGGCAAGAG
GATCATGCCACACCAAGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCCTAGCTAAC
GTTTACCCCTGCCCTGGGGCTGCAGCTGCGACCACATCCCAGGGTGGGTTAAAGATGAAC
TGCAACAAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCCAGCTCTAACGTGCAGGA
GCTTTCCCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACACACTTCAAG
AACCTTTGGACCTCAGGTGGTATACTGGATAGCAATTACCTGGACACGCTGTCCGGGA
GAAATTGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAAACAACCTG
CTGAGGTCCCTGCCTGTGGACGTGTTCGCTGGGTCTCGCTCTAAACTCAGCCTGCACAA
CAATTACTCATGTACCTCCGGTGGCAGGGGCTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGGAGTGCTCTGCACAATTGTGCCCTTCAAGCAGTGGGCA
GAACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTT
TAGAAAGGATTTCATGCTCCTCTCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACCTCGCACAGTAAAACAGCACTGGGTGGGGAGACCGGGACGCACTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTGGTGTGGGACTGCTGTGG
GTTTGTACCTCCGCCCTCACCGTGGGGCATGCTCGTGTGTTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCCCTCCGCTCCGAGATTAAATTCCCTACAGACAGTCTGT
GAACGCTTCCACTGGCACAATGGGCTTACAACGAGATGGGGCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTAAAGACCCCAACCCCAATAGGGAGGGCAGAGGGAAAGGCG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCCGCG
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTCGCACAAACGAAAGGGCT
GACCCCTTAAGTACGCTCCCTCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTCTTGCTGAGAGCCCCCTTGACAGAAAGCCCAGCACGACCCCTGCTGGAAG
AACTGACAGTGCCCTCGCCCTCGGCCCCGGGGCTGTGGGTTGGATGCCCGGTTCTATAC
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACCGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRIDPGAFQDLNKEVLILNDNLISTLPANVFQYVPITHLDLRG
NRLKTLPYEEVLEQIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLPPAPAQEETFAPGPLPTPKTNGQEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSDHIPGSGLKMNCCNNRNVSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLLDGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNQIQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNHYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSKNSTGLAETGTHNSYLDTSRVSISVL
VPGLL VFVTS AFTVVGMLV FILRNRKRSKRDANS SASEINS LQTV CDSSY WHNG PYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTCTCTGCGGGCTAAGGGAAACTGTTGGC
CGCTGGGCCGCGGGGGATTCTTGGCAGTTGGGGTCCGTGGGAGCGAGGGCGGAGGGG
AAGGGAGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCCTCGAGCGGACAGATCCAAGTTGGAGCAGCTGCGTGCAGGGCCTCAG
AGAATGAGGCCGGCGTTGCCCTGTGCCCTCTGGCAGGCGCTCTGGCCCGGGCGGCGG
CGCGAACACCCCCACTGCGGACCGTGTGGCTGCGCTGCCCTGGGGCCTGCTACAGCCTGC
ACACAGCTACCATGAAGCGGCAGGGCGCCGAGGAGGCTGCATCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCAGCTGCGCCTGTCGCTCGCCTCGGGCAGGCCAGG
GCCGGAGGGGCTCAAAGACCTGCTGTTCTGGTCGACTGGAGCGCAGGCGTTCCCAGT
GCACCCGGAGAACGAGCCTTGCGGGTTCTCCTGGCTGTCTCCGACCCGGCGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGGGAGATGCGC
GGTACTCCAGGCCACCGGTGGGTGAGCCGAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAAGTTGAGGTCTTGTGTCCTGCGCCGCCCGG
GCCGCTCTAACTTGAGCTATCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCGATGTGTTGTGCCCTGCC
GGGAGGTACCTCGTGGCAAATGCGCAGAGCTCCACTGCGCTAGACGACTTGGGAGG
CTTGCCTGCGAATGTGCTACGGCTCGAGCTGGGAAGGACGGCCGCTTGTGACCA
GTGGGAAGGACAGCCGACCCCTGGGGGACCGGGTGCCACCAGGCGCCGCCACT
GCAACCAGCCCCGTGCCGAGAGAACATGGCCAATCAGGGTCGACGAGAACGACTGGGAGAGAC
ACCACTTGTCCCTGAACAAGACAATTCAAGTAACATCTATTCTGAGATTCTCGATGGGAT
CACAGAGCACGATGTCTACCCCTCAAATGTCCCTCAAGCCGAGTCAGGCCACTATCACC
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTTCCTGCCACTCCTCAGGCTT
CGACTCCTCTCGCCGTGGCTTCATATTGTGAGCACAGCAGTAGTAGTGTGTTGGTATCT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCACGAAAGCCCTTCCAGCCA
AGGAAGGAGTCTATGGCCCGGGCTGGAGAGTGATCCTGAGCCGCTGCTTGGCTC
CAGTTCTGCACATTGCACAAACAATGGGTGAAAGTCGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCCTTGCTGGCGAGTCCCTTGGCTCTAGTGATGCA**ATAGGAAACAGGGGA**
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTGG
TGGTGAAGTGGGGACCGGGTAGTGTGCTGGGAGAGATATTCTTATGTTATTGGAGAA
TTTGGAGAAGTGATTGAACTTTCAAGACATTGAAACAAATAGAACACAATATAATTACA
TTAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT
ATTGGTTGAAATCCCAGGGAAAAAATAAAAATTAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLNEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPGA
ASNLNSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILTMVLGLVKLCFHESPSSQPR
KESMGPPGLESDEPAALGSSSAHCTNNGVKGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACCGCGTGGGATT CAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCAT AATCGCCTTAAAGTGCCTCCGCCCTGCCGGCGTATC
CCCCGGCTACCTGGGCCCGCCCCGGCGGTGCGCGCTGAGAGGGAGCGCGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCCAGTGTGAGCGGGCGGTGAGCGCGGTGGTGCAGGA
GGGGCGTGTGAGCCAGCGCTGCCAGTGTGAGCGGGCGGTGAGCGCGGTGGTGCAGGA
GGGGCGCGAACGCCCTGGCGCCACTCTGCCTGCTGGCTGCCACCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGGAAAATCA
CAGTTCCGAAGGAAAAGTAGTCGTTCAATTCCGATTCAAGACCTCGAGAGTGCACAAAC
CTGTGCCGCTATGACTTGTGGATGTGTACAATGCCATGCCAATGCCAGCGCATTGGCCG
CTTCTGTGGCATTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTCTTTAAAAC
CCCCAACTGGCCAGACCGGGATTACCCCTGCAGGAGTCATTGTGTGGCACATTGTAGGCC
CAAAGAATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGCCGGGAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGTAGTCCACCTGCACCAATTGTGTCTGAGAGAAATGAACCTCTTATTCA
TTTATCAGACTTAAGTTAACAGCAGATGGTTATTGGTCACTACATATTAGGCCAAA
AAACTGCCTACAACTACAGAACAGCCTGTCACCACCATCCCTGTAACCACGGGTTAAA
ACCCACCGTGGCTTGTCAACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTGTATTAGCCGGCACTGTTATCACAAACATCACTCGGATGGAGTTG
CACGCCACAGTCGATCATCACATCTACAAAGAGGGAAATTGGCGATTAGCAGGCCGG
CAAGAACATGAGTGCCAGGCTGACTGTCGCTGCAAGCAGTGCCCTCTCCTCAGAACAGGTC
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGAAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAACATCAGAACGCTCTGGATGCCCTAAAAATAAGCAATG
TTAACAGTGAACGTGTCATTAAAGCTGTATTCTGCCATTGCCCTTGAAGATCTATGTT
TCTCAGTAGAAAAAAATCTTATAAAATTACATATTCTGAAAGAGGATCCGAAAGATGG
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCCTCGAGATAGCTGAGGGAAAGTTCT
TGCCTGCTGTCAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCAGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAAGCGTTATTATACATCTCTGTAAGGAT
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTAGAAGTGCACATTAGT
GTTATTGTTCACCTCAAGCCTTGCCTGAGGTGTTACAATTGTCTTGCCTTCTA
AATCAATGCTTAATAAAATATTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGEVNDARRIGKYCGDSPPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRTGTLEGN
YCSSDFVLAGTVITTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCGCGGGCTGGGGCGGTGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTACACCTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACCATCCGGACAACCTTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTCGAGTGCCACCGCCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCTGC
CTTCCCTGTCTGGGGAACAGAGAGGCCCTGCGGTGGCTACGGCAGTGTGAAGGAGAACCG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGTGAGGCCTGTGGCC
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGGTATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGTCGGCACAGAGGGAGCCA
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGTTATCGCTGCATCTGTCGGCACAGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGCAGCAGATGTTCTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCAGTGGTTCACCGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTGTCAAGAGCAGTGGCTGGAGGGCTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCGAGAGCTTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTTGGTTATTGGAGAGTGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTCACCTGGCGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCTGCCAGTTCTGT
TCTGTGTTCACACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA
AAGGTCTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCGPAGTFGPSCLPCPGGTERPCGGYQCEGEGETRGGSGHCDCQAG
YGEACGQCGLGYFEAERNASHLVCACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLRSERDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-363

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGACTCTGGTGTGCCCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGGAGCCTGCTGCCAGCTGCAGCTAAAGAGGT
GCCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTCAAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGCCCTTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGCGCTGTCCCCGCCAGCGCCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCCGCACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCCTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTGGGGACTATGGAG
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGGCCAGAACTGGGTGCTGGAGCCCCCGGGCTT
CCTGGCTTATGAGTGTGGCACCCTGCCGGCAGCCCCCGGAGGCCCTGGCCTTAAGTGGC
CGTTTCTGGGCCCTGACAGTGCATGCCCTCGGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCTGGAGGAGGCTCCAGCCATAGGCGCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGTGAGGGTACCAAGGAGAGCTG
GCGATGACTGAACGTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTGGCTTCAGGAATGAGAATCTTGGCCACTGGA
GAGCCCTGCTCAGTTCTATTACTGCAGTATATTCTAACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTACTTGTCCGTAC
TGGATCTGGCTAAAGTCCACCACCACTCTGGACCTAACAGACCTGGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTTGAAAACATGAATAAAACACATTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSSLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWP
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGCGGCTGTTGTCAGTGGCCTGATCGCGATGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTCCTCTCATATTGGCGATCCTGTTGCTCCCTGG
CATTGGGCAGTGTACAGTCACACTCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGGAGTGGAGTTGACCA
AGGAGACACCAACCAGACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG
TGACCTTCTGCCA**ACTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC**
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATAACACACTGGTCAAAGAT
GGGATAGTGATGCCAACAGGAGAGCTGGTCTTGATCCCCTGTCA**GCCACTCTTCTATGTCT**
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCCTGTCA**GCCACTCTGATACTGGAGAATACA**
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGATGGAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCCCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAACCAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTACCGCCTATCATCTGCATTGCCCTACT
CAGGTGCTACGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCCTATTGTCTC
TACACCCCACAGGGCCCCCTACTTCTCGGATGTGTTTAATAATGTCAGCTATGCC
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACATTGTTAAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGCGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTCTGGCTCTTCCTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGG
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGTCTTCCATGGGAAGTG
CCACTGGATCCCTGCCCCCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGGAGCTTGTGGAGAGCATAGTAAATTTCAGAGAACATTGAAGCCAAAAG
GATTAAAACCGCTGCTCTAAAGAAAAGAAA**ACTGGAGGCTGGCGCAGTGGCTACGCC**
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGAGTTGGATCAGCCTGACCA
ACATGGAGAACCCACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAAGAGCAAAACTCCAGCTCAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW
KFDQGDTTRLCYNNKITASYEDRVTFLPTGITFKSVTREDTGYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIIPSSATIGNRAVLTSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTGPMTSNAVRMEAVERNVGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCCGAGCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG
GCTCGTGCACCCACCAAGTTCCAGTGCACCGACTGGCTTATGCGTGCCCCCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCCACGGCCA
CCCAGACTGTCCGACTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCACTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCAACACTGCCTATGGGTTATTGCAGCTGCTGCCGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTCTTTGTCCTGGCTCCGAGCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACAGAC
CTCGCTGCCCTGAGGACAAGCAACTTGCACCACCGTCACTCAGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLLLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLDLDCSDGSDEEECRIEPCQKGQCPPPGLPCPCTGVSDCSGGTDKKL
RNCSRLACIAGELRCTLSSDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPV
LESVTSLRNATTMGPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCACCGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGGAAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTCTAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTCAAGTGTGTGCTGACCCCGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGTTTCTTGAAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTCTATTATGTCGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCAAATGGTGAGTCACGGAGATTCTGTCT
GCCACCCGGCCTTGTGAGCGCTACAACCACCGAACTGTGGTGGAGTTTACTGCGATCCT
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGTTCCCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGGCTCCCCGGAG
TTCCAGCAGTGACCTGACTTGTGGTAGACGGCGTGCCTCATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCTTAGGCCCGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCTTACCCGTGGACGACCAGAGCCCCCAGCATAACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTGAGCTGCTCCAAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCTGCTGGACAACCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTAAAAATTCCAAAGTGTGCTGAAGTGTCTTTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTCTCTTGGTTAGACAAATGTAAACAA
AGCTCTGATCCTAAAATTGCTATGCTGATAGAGTGGTGGAGGGCTGGAAGCTTGATCAAGTC
CTGTTCTTCTGACACAGACTGATTAAAATTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKKGATKRLCLKHFNGLGWI PSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCACCGCGTCCGCTCCGCGCCCTCCCCCGCTCCCGTGCAGTCGCACGCCCTCTGCCGCCAGCCCGCTCCACCGCCGT
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGAAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGGTGGGCTGCCGGCGACGGGTGCCCTGCTGAGTGCC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTGTTA
TAAAGTCATTTACTTCCATGATACTTCTGAAGACTGAACCTTGAGGAAGCAAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTTCATTGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCGTGA
GGAGAAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT
ACAATTTAGGAACTGGTATGTGGATGAGCCGTCCTGCCAGGAGGTCTGCCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACAAATTCATTGCAAATATTCTGATGAGAAACAGCAGTCCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACAGCTGCCCTGAATCTGCCCTACAT
CCTAATCCCCAGCATTCCCTCTCCTCCTGTGGTCACCACAGTTGTATGTTGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAACACACCATC
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTCATTCCGAGTGTGTT
CGGGAGAAGCCACTCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGAGCGTGGAGAGTGAGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACAAATGGGAGGAGTAAGGAGTCTGGATGGTGAAATGAAATATATG
GTTATTAGGACATATAAAAACTGAAACTGACAACAAATGAAAAGAAATGATAAGCAAAATC
CTCTTATTTCTATAAGGAAAATACACAGAACGGTCTATGAACAAGCTTAGATCAGGTCTGT
GGATGAGCATGTGGCCCCACGACCTCCTGTTGGACCCCCACGTTGGCTGTATCCTTAT
CCCAGCCAGTCATCCAGCTGACCTTATGAGAACGGTACCTTGCCCAGGTCTGGCACATAGTA
GAGTCTCAATAAAATGCACTTGGTTGGTTGTATCTAACCTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGGCTGTGGAGCTGGAAAACCACCTCTGTTTCCCTGCTCTACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAACATCTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGGAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGQTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIKEFIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTPVLPETQEEDAKTFKESREAALNLAYILIPSIPLLLLLV
VTTVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSEGFTLVSVESGFVTNDIYEFSQDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCTACCACCATGATACTGGTGT
GTTCAAGCATGCGCTTGTGGACCCCAGTGGCGTCCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTTCGACACGGGCTCGGAGTCCTCTCAAGCC
GCTCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTGATTACACAGTCACCAATCTAGCTGGTGGTCCAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTTGGAGAGAGACTGAGGAAGAACTATGTGAAGACATTCCCTTTC
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCAAGACTTGTATCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGTATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGACTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCGGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG
TGACCTTCATACCGCTTTAATGACCTGGGATTTGACCACAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGAAATGAAGAGTAACTGATTAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPGVVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFIILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCP LD MF LNAMS VY TLSPE KY HAL CS QT QV M EV G NEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTTGCAGCTAAACTAAATATTGCTGCTGGGACCTCCTCTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGC GGCTGGTGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGACC GTGTGATG
ACGGCTGGACATTAAGGACGTGGCTGTGTTGCCGGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAACAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTCTTCTCCCCA
GTCCCAGAGGGTGTCA GGCTGGCTGACGGCCCTGGCATTGCAAGGGACGCGTGGAA GTGAA
GCACCAGAACCACTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCA TGCTCAGGACGAGAAGCAACCCTCA
GGATTGCCCTCTGGGCCTGGGGAAAGAACACCTGCAACC ATGATGAAGACACGTGGT CG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGAACCTCTGCTCTGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTCTGTGATGACA ACTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCCCTCCTCAGAGACCGGA
AATGCTATGCCCTGGGTTGGCCGCATCTGGCTGGATAATGTTGCTCAGGGAGGAG
CAGTCCCTGGAGCAGTGC CAGCACAGATTTGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGACTTATACTTGGTGCCCCTGATTCTCAGGCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGA ACTACATCA
CCACCTTCCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT
CAACTACTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCAATTGTCCTGTTCTGAGAAACTCTGACAAAATACAGATTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGGTTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTATTACAATAATAAGATAGCAC
TATGTGTTAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWECEDPFDLRLVG
GDNLCGSGRLLEVHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTGACCTCGAC
CCACCGTCCGGACCGTGGCGGACCGTGGCCGGCTACAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCCTGGG
CGTCTTCGGCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGCTATGTC
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACACCAGTGGA
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCAGTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA
CTGCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCAGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCAAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTGGCTGTTATCTCGAA
CTCTGGCTCCTGGCTCTTCTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGACTCTGACCAGCCAGGGCAGAGAAGCAGCACTTCTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTGTTGAGACTTTAATGGAGATTGCTCTACAAGTGGG
AAAGACTGAAGAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAGGGCGGCCGCACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCATGGCCCAACTTGTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI
VAAAEEILQCFGYVDIL
VNNAGISYRGTIMDTTDVVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCACCGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAATTTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGACTCCTCGTGAAGCTTTTATTCTAA
GAGGAGAAAATCAGTCACCGCGAAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GAATGACTGCCTATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGATATAAATAAG
CATGGACTGGAGAACAGCTGCCAATGCAAGGGACTGGTGCCAAGGTTACACCTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGACACATTCTGGACTACAAA
GGCATTCTCCTGCAATGACGAAGAATAACCATTGCCATATTGTCAGTGTGGCTCGGCAG
CTGGACATGTCTCGGTCCCCTCTTACTGGCTACTGTTCAAGCAAGTTGCTGTTGGA
TTTCATAAAACTTGACAGATGAACTGGCTGCCTACAAATACTGGAGTCAAAACAACATG
TCTGTGTCTAATTCGTAAACACTGGCTTCATCAAAATCCAAGTACAAGTTGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG
ATTTTATTCCATCTTCTATAGCTTTTAACAACATTGGAAAGGATCCTCCTGAGCGTT
CCTGGCAGTTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAAGCACCTAGTTCTGAAAATGATTACCAAGGTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTTAATGTTGAACTTCTGTTTTCTAATTATCCCCATTCTCAATA
TCATTTTGAGGCTTGGCAGTCTCATTACTACCACTTGTCTTAGCCAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTAGAGGTGACTTTAAGGAAAATGAAGAAAAGAA
CCAAAATGACTTTATTAAAATAATTCCAAGATTATTGTGGCTCACCTGAAGGCTTGCAA
AATTGTACCATAACCGTTATTAAACATATATTATTATTGTGGCTCACCTGAAGGCTTGCAA
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGGGTATTCAACATGAATATCATGAACTCTCAATGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACCTCACATTCAATGCCAAACATTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTAAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTAAAAAAA
AA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 58

MKFLLDILLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTTLDEAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCACCGCTCCGGACCGTGGTCGACTAGTTAGATCGCGAGCGGCCGCCGCGCTC
AGGGAGGAGCACCAGACTCGGCCGCACCCCTGAGAGAGATGGTGGTGCCTGTTGAAAGGTGATTG
TTTCGCTGGTCTGTTGATGCCCTGGCCCTGTGATGGCTGTTCGCTCCCTATACAGAAGT
GTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTCCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTGGTTC
TTCCCAGCTCAGATACAGCCAGAAGATGCCAGTAGTTCTCTGGCTACAGGGTGGGCCGG
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGCCCTATGTTGTCACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTACTGATGATAACCACGGATATGCAGTCAGTGAGGACGATGT
AGCACGGGATTATACAGTCACTAATTCAAGTTTCAGATATTCCTGAATATAAAAATA
ATGACTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGGCATTGCACACCTC
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCCGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT
TGTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCACTTAAC
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCAGGT
GCACGGAACCTGAGGATCAGCTTACTATGAAATTGGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGGAACATAGTTGAAAAGTACTTGCAGA
AGATACAGTACAGTCAGTTAAGCCATGGTTAATGAAATCATGAATAATTAAAGGTTCTGA
TCTACAATGCCAACTGGACATCATCGTGGCAGCTGCCGTGACAGAGCGCTCTGATGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGAATTCCATCAGGTAATTATTC
GAGGTGGAGGACATATTTACCCATGACCAGCCTGTGAGAGCTTGTACATGATTAATCGA
TTCATTTATGGAAAAGGATGGATCCTTATGTTGGATAAAACTACCTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCAAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTTACCAATAAAAATTATCCTGAAACAAAGTGAGC
TTTGTGTTGGGGAGATGTTACTACAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAAGATGTATAATGA
AATTTAGGGTCTTGAATAGGAAGTTAATTCTTCTAAGAGTAAGTGAAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTCTGCCATAACAGAAGTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA
TAGTTTGGGAAAAGATTCTCAAATGTATAAAGTCTAGAACAAAAGAATTCTTGAAATA
AAAATATTATATAAAAGTAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPKGDSGQPLFLTPYIEAGKIQKGREL
VGPPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLRDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHЛИHSLNПVREVKINLNГIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGLTSDPSYFQNVG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGНQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAЕKKVWKIFKSDSEVAGYIRO
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTCGGCTCCGAATGGCACATGTGGGAATCCCAGTCTTGGCTACAACAT
TTTCCCTTCTAACAAAGTCTAACAGCTGTTAACAGCTAGTGTACAGGGGTTCTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTT
CCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGCCTGCCTAACAAAGCTTCAAAAAACAGGAGCGACTTCACTGGGCTGGGAT
AAGACGTGCCGGTAGGATAGGAAAGACTGGGTTAGTCCTAACATTGACTGGCTGGG
TGAACCTAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTAACGGGCCAGAAA
TAGAGATGCTTGTAAAATAAATTTAAAAAAAGCAAGTATTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGGGAGAAAGTATGTTAAAATA
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACCCAGGATGGGACCCCTGGGTC
AGGCCAGCCTTTGCTCCTCCGGAAATTATTTGGTCTGACCACTCTGCCTTGTGTTT
GCAGAATCATGTGAGGGCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGCTCTCAGTGGCTGGGTGCTGGCCCCCCCAGCAGCCGGC
ATGCCCTCAGTTCAGCACCTTCACTCTGAGAACATCGTACTGGACCTTCAACCACCTGACCGT
CCACCAAGGGACGGGGCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCCCTCATCGTCAGCCCTGCAGCGAAGTGCTCACCTCACCAACAATGTCAACAAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGAGCCTTACCAAGGGGTCTGCA
AGCTGCTGGGCTGGATGACCTCTCATCCTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCAGTGTCAACAAGACGGGCACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATGGCACGGCTGGATGGGAAGCAGGATTACTTCCGACCCCTGTCCA
GCCGGAAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT
TTTGTCTCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCCACTTGACAT
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCGAGA
CCCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTTCTACACCTCACGCATCGTGC
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGCCCTGGCTGCACCCGGC
CGGGGTGGAATACGCCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGACTCACTGGGCC
AGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTGCCATCTCTCAAAGGGCAGAAG
CACTATCACCAACCGCCCGATGACTCTGCCCTGTGTGCCCTCCCTATCCGGGCATCAACTT
GCAGATCAAGGAGCCCTGCAGTCTGCTACCAAGGGCGAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGTCCAGTGCACGAAGGCGCTGTCCCCATCGATGATAACTCTGTGGA
CTGGACATCAACCAGCCCTGGAGGCTCAACTCCAGTGGAGGGCCTGACCCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTCAGATGCTCAAATGCC
ATTCACCTCTCAGCAAAGAGTCCCTTTGGAGGCTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTATTTCTGGGAACAAAGGTGAATGGGAGGTAAGAAGGGTTAATTTGTG
ACTTAGCTCTAGCTACTCCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCAAACTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLIIIDYSENRLLACGSL
YQGVCKLLRLDDLFLILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEGN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGGACTGGAGTGGAAACCGGGTCCCGCGCTTAGAGAACACCGCATGACCA
CGTGGAGCCTCCGGCGGAGGCCGGCCCGCACCGCTGGACTCCCTGCTGGCTGGCTCTGGGCTTCTGGCTCC
GCAGGCTGGACTGGAGCACCCCTGGCTCTGCGGCTCCGCATCGACAGCTGGGCTGCAGGCCAAGGGCTGA
ACTTCATGCTGGAGGATTCCACCTCTGGATCTCGGGGCTCCATCCACTATTCCTGTCAGGCCAAGGGACT
GGAGGGACCGCCTGCTGAAGATGAAGGCTGTGGCTTAACACCCCTACCCACCTATGTTCCGTGAAACCTGCATG
AGCCAGAAAGAGGCAAATTGACTTCTCTGGAACCTGGACCTGGAGGCTTCGTCCTGATGGCCAGAGATCG
GGCTGTGGGTGATTCTCGCTCCAGGCCCTACATCTGCACTGAGATGGACCTCGGGGCTTGCCAGCTGGCTAC
TCCAAGACCTGGCATGAGGCTGAGGACAACCTACAAGGGCTTACCGAAGCAGTGGACCTTATTGACCAC
TGATGTCAGGGTGGTGCACCTCCAGTACAAGCGTGGGGACCTATCATTGCGTGCAAGTGGAGAATGAATATG
GTTCCATAATAAAAGACCCCGCATACATGCCCTACGTCAGAAGGCACTGGAGGACCGTGGCATTGTGAACTGC
TCCTGACTTCAGACAAACAAGGATGGGCTGAGCAAGGGATTGTCAGGGACTCTGGCCACCATCAACTTGCACT
CAACACACGAGCTGCAGCTACTGACCACCTTCTCTCAACGTCAGGGACTCAGCCCAAGATGGTATGGAGT
ACTGGACGGGGTGGTTGACTCGTGGGGAGGGCCACAAATACTGGATTCTCTGAGGTTTGAAAACCGTGT
CTGCCATTGTGGACGCCGGCTCCATCAACCTCTACATGTTCCACGGGACCCAACCTTGGCTTCATGAATG
GAGCCATGCACTCCATGACTACAAGTCAGATGTCACCGCTATGACTATGATGTCGTGTCAGAAGGCCGCG
ATTACACGGCAAGTACATGAAGACTTCTCGGCTCCATCTCAGGCATCCCTCCCTCCCCCACCTG
ACCTCTTCCAAGATGCCATGAGCCCTAACGCCAGTCTTGACCTGCTCTGTCAGGGACGCCCTCAAGTACC
TGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCCT
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCACGTGCATGATGGGGCAGG
TGTTGTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATGTCGTGCCCCCTGATCCAGGGTT
ACACCGTGTGAGGATCTGGTGGAGATCGTGGCGAGTCACATGGGAGAATATTGATGACCAAGCGCAAAG
GCTTAATTGGAAATCTCTATCTGAATGATTCAACCTGAAAACCTCAGAACATCTATAGCCTGGATATGAAGAAGA
GCTTCTTCAGAGGTTGCCCTGGACAAATGGNGTCCCTCCAGAAACACCCACATTACCTGCTTCTTGG
GTAGCTGTCCATCAGCTCACGCCCTGTGACACCTTCTGAAGCTGGAGGGTGGAGAAGGGGTTGTATTCA
TCAATGCCAGAACCTTGGACGTTACTGGAACATTGGACCCAGAACAGCCTTACCTCCAGGTCCCTGGTTGA
GCAGCGGAATCAACCAGGTACCGTTTGAGGAGACGATGGCGGCCCTGCATTACAGTCAGGAAACCCCCC
ACCTGGGCAGGAACCAGTACATTAAAGTGGCGGTGGCACCCCTCCTGCTGGTGCAGTGGGAGACTGCCGCTC
CTCTGACCTGAAGCCTGGCTGCTGCCACCCCTCACTGCAAAGCATCTCTTAAGTAGCAACCTCAGGG
ACTGGGGCTACAGTCTGCCCTGTCTCAGCTCAAACCTAAGCCTGCAGGGAAAGGTGGATGGCTCTGGCC
TGGCTTGTGATGATGGCTTCTACAGCCCTGCTCTTGCGCGAGGCTGTCGGCTGTCTTAGGGTGGAGC
AGCTAATCAGATGCCAGCCTTGGCCCTCAGAAAAAGTGTGAAACAGTGCCTTGACCGGACGTACAGCCC
TGCAGCATCTGCTGGACTCAGCGTGTCTTGCTGGCTGGGAGGCTGGCACATCCCTCATGGCCCCAT
TTTATCCCCGAATCTGGGTGTGTCACCAAGTGTAGAGGGTGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCCTTACAACCTCTGAGCCTTCTTGGGATTCTGGAAGGAACCTGGCGTGGAGAACATGTGACTTCCCC
TCCCTTCCACTCGCTGCTTCCCACAGGGTACAGGCTGGCTGGAGAACAGAAATCCTCACCCCTGCGTCTCC
CAAGTTAGCAGGTGTCTGGTGTTCAGTGAGGAGGACATGTGAGTCCTGGCAGAACGCATGGCCATGTCTGCA
CATCCAGGGAGGAGGACAGAACGCCAGCTCACATGTGAGTCCTGGCAGAACGCATGGCCATGTCTGACATCC
AGGGAGGAGGACAGAACGCCAGCTCACATGTGAGTCCTGGCAGAACGCATGGCCATGTCTGACATCCAGGG
GGAGGACAGAACGCCAGCTCACATGTGAGTCCTGGCAGAACGCATGGCCATGTCTGACATCCAGGGAGGAGG
ACAGAACGCCAGCTCACATGTGAGTCCTGGCAGAACGCAGGGGAGGACAGCACCCCTGCGTCTGGCTACTGCTG
GAAGTGTGTCAGTCCGATTTGAGCCTTGTCTGGGGCCAGCCAAACACCTGGCTGGCTACTGCTG
GTTGAGTAAAGCTATAACCTTGAATCACAA

FIGURE 64

MTTWSLRRR PARTLGLLLL VV LGFLV LRR LDW STLVPL RL RHRQL GLQAK GWN FM LED STFW
I FGGS I HYF RV PREY WR DR LL K MKAC GLN T LTT Y VP WNL H E PERG K F D FSG NLD LEAF VL MA
AE I GLW V I L R PGP Y I C S E M D L G G L P S W L L Q D P G M R L R T T Y K G F T E A V D L Y F D H L M S R V V P L Q
Y K R G G P I I A V Q V E N E Y G S Y N K D P A Y M P Y V K K A L E D R G I V E L L L T S D N K D G L S K G I V Q G V I A T
I N L Q S T H E L Q L L T T F L F N V Q G T Q P K M V M E Y W T G W F D S W G G P H N I L D S S E V L K T V S A I V D A G S
S I N L Y M F H G G T N F G F M N G A M H F H D Y K S D V T S Y D Y D A V L T E A G D Y T A K Y M K L R D F F G S I S G I P
L P P P P D L L P K M P Y E P L T P V L Y L S L W D A L K Y L G E P I K S E K P I N M E N L P V N G G N G Q S F G Y I L Y E
T S I T S S G I L S G H V H D R G Q V F V N T V S I G F L D Y K T T K I A V P L I Q G Y T V L R I L V E N R G R V N Y G E N
I D D Q R K G L I G N L Y L N D S P L K N F R I Y S L D M K K S F F Q R F G L D K W X S L P E T P T L P A F F L G S L S I S
S T P C D T F L K L E G W E K G V V F I N G Q N L G R Y W N I G P Q K T L Y L P G P W L S S G I N Q V I V F E E T M A G P A
L Q F T E T P H L G R N Q Y I K

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
CTGGTGAGGGTCTCTACTTGGCCTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGCTCGGCCGAGGCCCGAGGACCTCCATCTCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCC**ATGGCTCCC**
AAGAAGCTGTCCTGCCTTCGTTCCCTGCTGCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTCGTCGTTAGTGGATAGGGGTATGACCGGTTCTCCTAGACGGGGCC
CGTCCGCTATGTGTCTGGCAGCCTGCACTACTTCCGGTACCGCGGGTCTTGGGCCAC
CGGCTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGACCTCATTGCCTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCCATCCTGGTTGCTCGAAAACCTGAAATTCTATCTAAGAACCTC
AGATCCAGACTTCCTGCCGAGTGGACTCTGGTTCAAGGTCTGCTGCCCAAGATATATC
CATGGCTTATCACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTCAGTACATGAGGCACCTGGCTGGGCTTCCGTGACTGCTAGG
AGAAAAGATCTGCTCTCACACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GACTCTATACCACTGTAGATTGGCCCATGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
CGGAAGTATGAACCCCATGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
CTGGGCCAGAATCACTCCACACGGCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGATATTGG
AATGGTGCCGATAAGAAGGGACGCTCCTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCCACACCTAACGCTTTGCTCTCGAGATGTCATCAGCAAGT
TCCAGGAAGTTCTTGGACCTTACCTCCCCGAGCCCCAAGATGATGCTGGACCTGTG
ACTCTGCACCTGGTTGGCATTACTGGCTTCCTAGACTTGCTTGGCCCCGTGGGCCAT
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGTACC
GAACCTATATGACCCATACCATTTTGAGCCAACACCATCTGGTGCCAAATAATGGAGTC
CATGACCGTGCCTATGTGATGGATGGGTCCAGGGTGTGAGCAGAATATGAG
AGACAAACTATTTGACGGGAAACTGGGTCCAAACTGGATATCTGGTGAGAACATGG
GGAGGCTCAGCTTGGTCTAACAGCAGTGAACAGCAGGCTGTTGAAGCCACCAATTCTG
GGCAAACAATCCTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG
GTGGTTCCCTCCAGTTGCCAAAATGCCATATCCTCAAGCTCCTCTGGCCCCACATTCT
ACTCCAAAACATTCCAATTAGGCTCAGTGGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGGTTAACCTGGCCGGTACTGGACAAAGCAGGGCC
ACAACAGACCCCTCACGTGCCAAGATCCTGCTGTTCTAGGGAGCCCTAACAAAATTA
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGCACT**GTAAAGGTAGGCCGGCATGGTGGCTCATGC**
CTGTAATCCAGCAGTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAGGACTTCAAGA
CCAGCCTGGCCAACATGGTAAACCCCGTCTCCACTAAAAAATACAAAAATTAGCCGGCGTG
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
AGGAGGCAGAGGTTGCAGTGGAGGTTGTACCACTGCACCTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGILPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFSYMRHLAGLFALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQNHSTRSAVTKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFALRDVISKFQEVPGLPPPSPKMMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMHTIFEPTFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTGAAACACGCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACCTTGAGGAATATT
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAACGATTT
GCGTCCCTCTTACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGAGTTAGTGAAAATAACTTAGGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGGTGCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAAACAGACTGCTTTAGCTTCTCGCGATCACTTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGGTGTATTGCTCAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTCTATAATGACGGCAC
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA
ACTGTGAGCTAGAGAGAACCCACATGCTATTTCAGCCTCTCTAACAGGAACGGAT
TTAAAGTCCAATAACATTGCACAATTGAGGAAATCATCAGTTCCAGCATTAAAAGACT
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCTATTACCCATGTCA
AAAACTTGGAGTCACTTATTCTCTAACACAACAGCTCGAACCTTACCAAGTGGAGTATT
AGTTACAGAAAATCAGATGCTTAGATGTGAGCTACAACAAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC
CAAACAAATTGTTAAATGCATAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC
TCACCTCCAGAGAAAGTTGGTCAGCTCTCCCAGCTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAGATCACCTTTGATAACCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAAATGGGATTTAACTAAGATAATATATGACAGTGATGTGCAGGAAC
AACTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGTAGGGTTTAAGTCATTCAACATTGAAATCATTGTTTTCTTTGGGG
AAAGGGAAAGGAAAATTATAATCAATCTGGTTCTTTAAATTGTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTGCCGTCAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG
VPDAVFDTLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMICLQELRHLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTKLVLNLSLKKMMNVAELELQNCELERIPIHAIFSLSNLQELDLKS
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCLDRLPAQLGQCRMLKKSGLVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACACGCGTCCGGCCTTCTCTGGACTTGCATTCCATTCTTTCATGACAAACTGACTTTTTATTC
TTTTTCCATCTCTGGGCAGCTGGATCCTAGGCCCTGGAAAGACATTGTGTTTACACACATAAGGAT
CTGTGTTGGGTTCTTCTCCTCCCCTGACATTGGCATTGCTTAGTGGTTGTGGGGAGGGAGACCACGTGG
GTCAGTGCTTGCTTGACTTATCTGCCTAGGTACATCGAAGTCTTGACCTCCATACAGTATTATGCCTGTC
ATCGCTGGTGTATCCTGGCGCTGCTCCTGCTGATAGTTGTCGTCTGTCTTACTTCAAAATACACAAAC
GCGCTAAAAGCTGCAAAGAACCTGAAGCTGTTGCTGAAAAATCACAAACCAAGACAAGGTGTGGTGGGCAAG
AACAGCCAGGCCAAACCAATTGCCACGGAGCTTGTGCTGACATAAATGAGGCCCTGAGTTAGGAAAGGCTCCCTCTCAA
AGTTTGATTCCCTGCCACCTTGCTGCGACATAAATGAGGCCCTGAGTTAGGAAAGGCTCCCTCTCAA
GCAGAGCCCTGAAGACTTCAATGATGTCATGAGGCCCTGTTGTGATGTCAGGCCACAGAAGAAAGGCACAG
CTCCCCATCAGTTCATGAAAATAACTCAGTGCTGCTGGAAACAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGCAACCCCTCAGGAAGGAGTGGGGAGAGAACCCCTACTGTGGGAATGCTGATAAACAGTCA
CACAGCTGCTCTATTCTCACACAAATCTACCCCTGCGTGGCTGAACTGACGTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCTATAAAAGCTGTCGGCTTAAGGCTGCCAGGCCCTGCAAATGGAGCTTGA
AGAAGGCTCATGCCATTGACCCCTTAATTCTCCTGTTGGCGAGCTGACAATGGGGAGGCTGAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGTGCAAATATGGCAGAGACCCACAAGGCCATGATCCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAGACCAAGAAAACAAAGCATCAGAATTATCTTCTATGTCCAGCTT
GATCCAGATGGAAGCTGAAAGTGAACATTAAGCTTTGACGGAACCTCCAGCAATGGGCTCTGCTAGGG
CAAGTCTGCAGTAAAAGCACTATGTCCTGATTGAAATCATCATCCAGTACATTGACGTTCAAATAGTTACT
GAECTCAGCAAGAATTCAAAGAACTGTCCTTGCTTCACTACTTCTCTCCTAACTCTCTATTCCAAACTGT
GGCGTTACCTGGATACCTTGGAGGATCCTCACCGCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT
TGTGTTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTAACTCAAAGAGATTTCCTAGAAATAGAC
AAACAGTGCACATTGATTCTTGCATCTATGATGGCCCTCCACCAACTCTGGCTGATTGGACAAGTCTGT
GGCGGTGTGACTCCCACCTCGAATCGTCATCAAACCTCTGACTGTCGTGTTGCTACAGATTATGCCAATTCT
TACCGGGGATTCTGCTCCTACACCTCAATTATGAGAAAACATCAACACTACATCTTAACTTGCCTTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACAGAGGTTTAACTCTAATGGGATAACTTGCAACTAAA
GACCCAACCTGCAGACCAAAATTATCAAATGTTGGAATTCTGTCCTCTTAAATGGATGTTGACAATCAGA
AAGGTAGAAGATCAGTCACATTACACCAATAATCACCTTCTGATCCTCTCAACTCTGAACTGATCACC
CGTCAGAAACAACTCCAGATTATGTAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATAACATAACA
GAAGATGATGTAATACAAAGTCAAATGCACTGGGAAATAACACAGCATGGCTTTGAAATCCAATTCA
TTTGGAAAAGACTTACCTGAAATCACCATATTATGTTGAGGTTGAAACCAACTCTTGTCAAGTTAGTCTGCAC
ACCTCAGATCAAATTGTTGTTCTGATACCTGAGGCCCTCCACCTCTGACTTTGCATCTCCAAACC
TACGACCTAATCAAGAGTGGATGTAAGTGTGAGGATGAAACTTGTAAAGGTGATCCCTTATTGGACACTATGGGAGA
TTCCAGTTAATGCCCTTAAATTCTGAGAAGTATGAGCTGTGTTGATCTGCAGTGTAAAGTTGATATGTGAT
AGCAGTGCACCAAGTCTCGCTGCAATCAAGGTTGTCCTCCAGAAGCAAACGAGACATTCTCATATAATGG
AAAACAGATTCCATCATAGGACCCATTGCTGAAAAGGGATGCAAGTGCAGTGGCAATTCAAGGATTCAGCAT
GAAACACATGCCAGAAACTCCAAACCAAGGCCCTCAACAGTGTGCACTGTTCTCATGGTCTAGCTCTG
AATGTGGTGAATGTCAGCGACAATCACAGTGAGGCTTTGAAATCAACGGGAGACTACAAATACAGAAGCTG
CAGAACTATTAACTAACAGGTCAAACCCCTAAGTGGAGACATGTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTGAATAATGAGGAAGGGCTGAAAGTGACACACAGGCCCTGATGAAAAAAA

FIGURE 70

MELVRRLMPLTLIILSCLAE LTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLQVCSKNDYVPVFESSSSTLT
FQIVTDSARIQRTVFYYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVGRVTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSIYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTIILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNNAFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVRSKRDIISSYKWKTDIIGPIRLKDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCTGCGCCG
GGACATGCGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCAGTGTGCTGTTGCTGCTGC
TGCTGCCGCCGCCGTGCCCTGCCACAGCGCCACGCCAGTGTGCTGACCCCACCTGGAGTCC
CTGGACGCCGCCAGCTGCCCGCGTGGTTGACCAGGCCAAGTTCGGCATCTCATCCACTG
GGGAGTGTGTTCCGTGCCAGCTCGGTAGCGAGTGGTCTGGTGTATTGGAAAAGGAAA
AGATACCGAAGTATGTGAAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT
TTGGACCACTATTACAGAAAATTAAATGCCAACAGTGGCAGATATTTCAGGC
CTCTGGTCCAATACATTGTCTTAACCTCAAACATCATGAAGGCTTACCTTGTTGGGGT
CAGAATATTGTGAACTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGAACAGAACTGACCTGCCTTGGACTGTACTATTCCCTTTGA
ATGGTTCATCCGCTTCTGAGGATGAATCCAGTCATTCCATAAGCGGAATTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACGGATCAATACTGGAACAGCACAGGCTCTGGCCTGGTT
ATATAATGAAAGCCCAGTCGGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTACCTGCAGTGATCGTTATAACCCAGGACATCTTGCCA
CATAAAATGGAAAATGCATGACAATAGACAAACTGTCCTGGGCTATAGGAGGAAAGCTGG
AATCTCTGACTATCTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTCATGTG
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTTCTGTAGTTTGAG
GAGCGACTGAGGCAAGTGGGCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTCTAAATGGCCACATCAGGACAGCTGTTCTGGCCAT
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAAC
GATTCTTGGAGAAAATGGCATTATGGTAGAACTGCCACAGCTAACCAATTCAAGATGC
CGTGTAAATGGGCTGGCTAGCCCTAACTAATGTGATCTAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAACGGATAAGAAAATTATTGGCAGTCAGCCCTTCCCTTTCCACTA
AATTCTTCTAAATTACCCATGTAACCATTAACTCTCCAGTGCACTTGCCATTAAAGTC
TCTTCACATTGATTGTTCCATGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTATGTTGAAGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAT
TTTTTTGTGCCAACATCATAGAGTGTATTACAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATACAGCATGTTACTG
AAACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGAAACATAGAGAAG
GTACAGTAAAATACTGTAAAATGGTGCACCTGTATAGGGCACTTACCCAGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAATCTGTATGCTTAGGCTACACTACATTATAAAAAAAA
GTTTTCTTCTCAATTATAAACATAAGTGTACTGTAACTTACAAACGTTAAATT
TTTAAACCTTTGGCTTTGTAATAACACTTAGCTAAACATAAAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIFIHWG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHEGFTLWGSEYSWNNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETY
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWLALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTCCATCTGGACCACGAGGCTCTGGTCCAAGGCTTTGCCTGCAGAAGAGCT
TTCCATCCAGGTGTATGCAGAATTATGGGGATCACCCCTGTGAGCAAAAGGCGAACAGC
AGCTGAATTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCGGCAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTTGAGCTATGGCTGGGTGGAGA
TGGATTCTGGTCATCTCTAGGATTAGCCAAACCCCAAGTGTGGAAAAATGGGGTGGGTG
TCCTGATTTGAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACATCTGAT
ACTTGGACTAACTCGTCATTCCAGAAATTATCACCAACAAAGATCCCATTCAACACTCA
AACTGCAACACAAACAGAATTATTGTCACTGACAGTACCTACTCGGTGGCATCCCCCT
ACTCTACAATACCTGCCCTACTACTACTCCTCTGCTCCAGCTCCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTACAGAAGTTTATGAAACTAGCACCATGTCTACAGAAC
TGAACCATTGTTGAAAATAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGCAGCTGGTCTTGGATTTGC
TATGTCAAAAGGTATGTGAAGGCCTTCCCTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCATGATAGCAACCTTAATGAGGAATCAAAGA
AAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCCTGGAA
GCTGAAGTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCAGCTGGGAAATCAAAGGCCAAAGAACCAAAGAAGAAAGTCCACCCCT
GGTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAAC
CCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC
TTCTAGCCTGGCTATGCTTAATAATATCCCACGGAGAAAGGAGTTTGCAAAGTGCAA
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTGAGGCTAGG
TGGGTGAAAGCCAAGGAGTCACTGAGACCAAGGTTCTACTGATTCCGAGCTCAGAC
CCTTCTCAGCTCTGAAAGAGAACACGTATCCCACCTGACATGTCCTCTGAGCCCGGTA
AGAGCAAAAGAACATGGCAGAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAGCTAAAATAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAACACAGACAGGGTCAAAGTGTGTTCTCTGAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTCTCT
AGGAAATATACTTTACAAGTAACAAAAATAAAACTCTTATAAATTCTATTCTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCCTCAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTCT
GTTTGATATTCTAGCTTACTTCCAAACTAATTCTATTGCTGAGACTAATCTT
ATTCAATTCTCTAATATGGCAACCATTATAACCTTAATTATTAAACATACCTAACAGAAC
TACATTGTTACCTCTATATACCAAAGCACATTAAAGTGCCTTAACAAATGTATCCTA
GCCCTCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA
AGCATTAGAAAATT

FIGURE 74

MARCFSLVLLLTSIWTTTRLLVQ GSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISP NPKCGKNGVGVLIWKVPVSRQF
AA YCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTGGCACCTCTAATTGCTCTCGTATTGGTGCACGACTTCACGATGG
CTCGCCCAACCTTACTACCTCTGTGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA
ACTGCCGCCGCTCTGCCACGGCTGCCACCCAACGCGAAGACGGTAACCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCCAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTGGATTGTGGAGTTCTTGCAA
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTGGAAAGGTGGATGTTGGACGCTACTGATGTTAGTACGGTAC
AAAGTGAGCACATCACCCTCACCAAGCAACTCCCTACCCCTGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACCAAGTGTCA
TGGGAAAACAAGAAGGATAAAAGATCCTCACTTGGCAGTGCTCCCTCTCCTGTCATT
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTTAAAGAGGCATCTAGGAATTGTCAG
GCACCCTACAGGAAGGCCTGCCATGCTGTGGCCAAGTGTTCAGGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGGAAATGGTTCCCTCCAAGCTGGTCAGTGTGTTAAGTCTTAC
AGCTATTAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCCCTTTAG
TTGACCTGCACAGCTGGTTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCCTTCAAGGACTCTGCTTCTTAAGCCCTCTGGCTCGTTATGGTC
TTCATTAAAGTATAAGCCTAACTTGTGCTAGTCCTAAGGAGAACCTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTTGTGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGTGGTAGGACTGGAGGAGAACCTGGACTTCAC
TAACCCCTCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGGGCCCCGAGAGCTAGCCGTCGAGGAGCTGCCTGGGACGTTGCCCTG
GGGCCCCAGCCTGGCCGGTCACCCCTGGCATGAGGAGATGGCCTGTTGCTCCTGGTCCCA
TTGCTCCTGCTGCCGGCTCCTACGGACTGCCCTCTACAACGGCTTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTACGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCCTGTTCACCTACCAAGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGGCGGTGTGCGTGTCAAATGGTGGAAAGCT
GTCGGAGAACGGGCCCCAGAGAACGGACGTGCTGGTGGCCATCGGCTGAGGCACCGCTCCT
TTGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTCAATTGACGGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCCGGGTGTGGCTTTCTTACCAAGTCCCCCA
ACGGCGCTACCAGTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCCGTG
GTGGCCTCTTGAGCAGCTCTCCGGGCCTGGGAGGGAGGGCTGGACTGGTGCAACGCCGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGCAGCCCTGCCGTGACCGCTATGAT
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCGCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCCCTGAGAACGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGGAC
AGCTCTTGCCGCCTGGAAAGTCCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCCTGTGGTTACCCGCATCCTAACTGTGGGCCCCAGAGCCTGGG
CCGAAGCTTGGCTCCCCGACCCGCAGAGCCGTTGTACGGTGTACTGCTACCGCCAGC
ACTAGGACCTGGGCCCTCCCTGCCGATTCCCTCACTGGCTGTTATTGAGTGGTT
CGTTTCCCTGTGGTTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTCT
TTAACATTTTACTATTTTGAAAGCAACAGAACCCATGCCCTCCCTTGCTCCTG
GATGCCCACTCCAGGAATCATGCTGCTCCCTGGGCCATTGCGGTTTGCGGCTTCTG
GAGGGTCCCCGCCATCCAGGCTGGCTCCCTCCCTTAAGGAGGTTGGTGGCCAGAGTGGG
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGGCATGGTGGGCACAGTTCTCCCTGCC
CAGCCTGGGGAAGAACGGCCTGGGGCCTCCGGAGCTGGCTTGGCCTCTCCTGCC
CACCTCTACTCTGTGAAGCCGCTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTCCAGGCAGGAAATCTGAGGAAAGGAAGAAACTCCCTCCCCGTTCC
TCCCTCTCGGTTCAAAGAACATCTGTTGTCATTGTTCTCCTGTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGCTATGACTGCCCTCCGCCAA
AA
AA

FIGURE 78

MGLLLVPLLLPGSYGLPYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFVQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGP
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSDAGPHQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDGRVGWEELRNATYGHYAPGEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKDGHLDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCAGGGCGCGGGTGCAGGGGATCCCTGACGCCTCTGTCCCTGTTCTTGTGCTCCCAG
CCTGTCTGTCGTCGTTGGCGCCCCCGCCTCCCCCGGGTGCAGGGGATCCGACACCGATCCTG
GGCTTCGCTCGATTGCGCCGAGGGCGCTCCAGACCTAGAGGGCGCTGGCTGGAGCAG
CGGGTCGTCGTTGTCCTCTCCCTCTGCAGCCGCCCCGGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGTGACGCGCGGGCTCCCGCACCTGGCCTGCCCATTCTCCCTCTCCAG
GTGTGAGCAGCCTATCAGTCACCATGTCCGAGCCTGGATCCGGCTCTCGGCCTCGGTGTG
TGTCTGCTGCTGCTGCCGGGGCCCGGGCAGCGAGGGAGGCCCTCCATTGCTATCACATG
TTTACAGAGGCTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGCTGCC
CTCTGAGGAATTCTGTGATGGAACATAGTATGCTCTGTATCGAGCATATGTGGG
GCTGCTGTCACAGGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAACATTCCCTAGTAGATGCCATGGCATCCAGTCTCAAATGCTTCTAGAT
GGTCTGCTCTTCACAGTAACTAAAGGAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCACAGCACATCCACCAACAGGTAAACAGACTAAAGAAAACACCCGAGAAGAAAAC
CAATAAAGATTGTAAGCAGACATTGCATTCTGATTGATGGAAGCTTAATATTGGCAGC
GCCGATTTAATTACAGAAGAATTGTTGGAAAAGTGGCTCTAATGTTGGAAATTGGAACA
GAAGGACCACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATTACTTGAA
AAACTTACATCAGCAAAGATGTTGTTGCCATAAAGGAAGTAGGTTAGCAGAGGGGTA
ATTCCAATACAGGAAAAGCCTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGATCCCCAAAGTGGTGGTATTATTGATGGTGGCCTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGCTGT
CGGAATAATGGCTTCTCTTACCATGCCACTGGTTGGCACCAAAATACGTAAA
GCCTCTGGTACAGAAGCTGCACTCATGAACAAATGATGTGCAAGACCTGTTATAACT
CAGTGAACATTGCCTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCC
ATGCTGAAATTGTTCCAACATAGCCAAGACTTTGAAATCTCGGACATTGGTCCAAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCACTGACTATAGCACCA
AAGAGAATGTCCTAGCTGTCACTAGAAACATCCGCTATATGAGTGGTGAACAGCTACTGG
GATGCCATTCTTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCAGGCTGCAAGCTGCTG
CACATGATGCAGGAATCACTATCTCTGTGTTGGCTGGCCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTCTTACAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGTTAGAGATTCTTAGAATCCCAGCAAT
AAATGGTAACATTGACAACAGAAAGAAAAAGTACAAGGGGATCCAGTGTGAAATTGTATT
CTCATAACTGAAATGCTTCTGATCAGACATAGAATCAGATAACAAACTATTAAGTATGTCAC
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTCTGGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAAACCTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAA
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLLEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDKCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCCGCGCTCCCGCACCGCGGCCACCGCGCCGCTCCGCATCTGCACCCGCAGGCC
GGCGGCCTCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTC
GGGCGGCGCTGCGGGCGCAGAGCGGAGATGCAGCGGCTGGGGCACCCCTGCTGTGCCTGC
TGCTGGCGGGCGGCTCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCCGGCCGGCTCTCAGCTACCCGAGGAGGACACGCAGCACAAATTGCGCAGCGCGTGGAAAGAGATGGAGG
GGTGAGGAAGTGTGGAGGACACGCAGCACAAATTGCGCAGCGCGTGGAAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACACTACCTCCAGCTAT
CACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTCATCATCGACGAGGACTGTGGGCCAGC
ATGTAAGTGCAGTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCGGGCTG
TGCTGTGCCTCCAGAGAGGGCTGCTGTTCCCTGTGTGCACACCCCTGCCGTGGAGGGCGA
GCTTGCATGACCCGCCAGCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTGTGCCAGTGGCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTTCGTGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGCCAGCTTCATGGAGGAGGTGCCAGGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCAGCGCCGCT
GCACTGCTGGAGGGAAAGAGATTAGATCTGGACCAAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTTCCCCAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCTTACA
TCTTCTTCCCAGTAAGTTCCCCTCTGGCTTGACAGCATGAGGTGTTGCAATTGTTCA
TCCCCCAGGCTGTTCTCCAGGCTTCAGCTGGCTTGGGAGAGTCAGGCAGGGTTAAC
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACAGTTGGCAG
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTGTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAAACATCAA
CCTGGCAAAATGCAACAAATGAATTTCACCGCAGTTCTTCCATGGCATAGTAAGCTG
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACCTGCATTACATGTGTTATTCA
AGCAGTGTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGAGGGGTCAATTGTTCTCCTCGCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCA
CTGGTTGTGACTCTAAGCTCAGTGCTCTCCACTACCCACACCAGCCTTGGTGCCACCAA
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTTTCTTGAGGCATGCACATCTGGAATTAAG
GTCAAACTAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGAGCCGCTTCTAATGAAGACAATGATATTGACACTGTCCCTCTTGGCAGT
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATAACAGGTTAACCTGCAGAAACA
GTACTTAGGTAATTGAGGGCAGGATTATAAAATGAAATTGCAAATCACTTAGCAGCAAC
TGAAGACAATTATCACCAACACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT
GTAATATGCGACTGCCAACACTGAACCTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTGATCCAGAGTTCTTAAAGTTAAAGTTGACATGATTGTA
TAAGCATGTTCTTGAGTTAAATTATGTATAAACATAAGTGCATTAGAAATCAAGC
ATAAAATCACTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLPPSYHNETNTDTKVGNNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVROELEDLERSLTEEMALGEAAAAALLGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGGCTGGGAGGAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTAGAAGGACTCTG
AAGATAACAATAATTTCAGCCCATCCACTCTCCTTCCCTCCAAACACACATGTGCATGTACACACACATACA
CACACATACACCTTCCCTCCCTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTATAGAAAAGGACAC
TAAAGCCTTAAGGCAGGGCTGGCCATTACCTCTGCAGCTCTGGCTTGAGTCAAAAAACATGGGAGGG
CCAGGCACGGTGAACACCTGTAATCCCAGCATTGGGAGACCGAGGTGAGCAGATCACTTGAGGTAGGG
TTCGAGGACGGCTGGCCAAACATGGAGAAACCCCCATCTACTAAAAATACAAAAATTAGCCAGGAGTGGTGGC
AGGTGCCTGTAATCCCAGCTACGGTGGCTGAGGCCAGGAGAATCGCTGAAATCCAGGAGGGAGATGCAGT
CAGCTGAGTGCACCGCTGCACTCCAGCCTGGGTGACAGAAATGAGACTCTGTCTCAAACAAACACGGGAGGA
GGGGTAGATACTGCTTCTGCAACCTCTTAACCTGCACTCTGCTCTTCTCCAGGGCTGCCCCCTGATGGGGCCTG
GCAATGACTGAGCAGGCCAGAGGACAAGGAAGAGGATATTGAGGAGGGCAAGAAGTGAACGCCCG
GTGTTAGAATGACTGCCCTGGGAGGGTGGTCCCTGGGCCCTGGCAGGGTTGCTGACCCCTAACCTGCAAAACAC
AAGAGCAGGACTCCAGACTCTCCTGTGAATGGTCCCCCTGCAAGCTCACCATGAGGCTTCTCGTGGCCCC
ACTCTGCTAGCTGGGTGGCTGGCACTGCCACTGTGCCCTGGTACCCCTGGCATGTTCCCTGCCCCCTCA
GTGTGCCCTGCCAGATCCGGCCCTGGTATACGCCCGCTGCTCTACCGCGAGGCTACCACTGTGGACTGCAATGA
CCTATTCTGACGGCAGTCCCCCGGCACTCCCCGAGGCACACAGACCCCTGCTCTGAGAGCAACAGCATTGT
CCGTGTGGACCAGAGTGAAGCTGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTCGGA
TGCCCGAGACTGTGATTCCATGCCCTGCCAGCTGCTGAGCCTGACCTAGAGGAGAACAGCTGACCGGCT
GGAGGACCACAGCTTGAGGGCTGGCCAGCCTACAGGAACCTATCTCAACCACAACCAGCTCACCGCATCGC
CCCCAGGGCCTTTCTGGCTCAGCAACTTGTGCGGCTGCACCTCAACTCCAACCTCTGAGGGCCATTGACAG
CCGCTGGTTGAAATGCTGCCAACTTGGAGATACTCATGATTGGGGCAACAAGGTAGATGCCATCCTGGACAT
GAACCTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTCTAGCAGGCATGAACCTGCGGGAGATCTCGACTATGC
CCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCCTCTATGACAACCAGCTGCCCGGGTGCCAGGCGGGCACT
GGAACAGGTGCCGGCTCAAGTTCTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGACTTGC
CAACATGCTGACCTTAAGGAGCTGGACTGAACAACATGGAGGAGCTGGTCTCCATGACAAGTTGCCCTGGT
GAACCTCCCCGAGCTGACCAAGCTGGACATACCAATAACCCACGGCTGTCTTCATCCACCCCCGGCCTTCCA
CCACCTGCCAGATGGAGAACCTCATGCTCAACAACACGCTCTCAGTGCCCTGACCCAGCAGACGGTGGAGTC
CCTGCCCAACCTGCAAGGGTAGGTCTCCACGGCAACCCCATCCGCTGTGACTGTCTCATCGCTGGGCAATGC
CACGGGCCCCGTGTCGCTTACAGCCGAATCCACCCCTGTGCGGAGGCTCCAGCAGCGCCTCCC
GGTCCGTGAGGTGCCCTTCCGGAGATGACGGGACCACTGTTGCCCTCATCTCCCCAGAAGCTTCCCCCAAG
CCTCAGGTAGGGAGAGGACATGGTGTGCAATTGGGGCAACTGCCAACCCGAGATCTACTG
GGTCACTCCAGCTGGCTCGACTGACACCTGCCATGCAAGGAGGTACGGGTACCCCGAGGGACCC
GGAGCTGCGGAGGGTGACAGCAGAACAGGGCAGGGCTATACACCTGTGTTGGCCAGAACCTGGTGGGGCTGACAC
TAAGACGGTTAGTGTGGTGTGGCCGTCTCCTCCAGCCAGGAGGAAGGACAGGGCTGGAGCTCCG
GGTGCAGGAGAACCCACCCCTACACATCCTGCTATCTGGGTCAACCCACCAACAGTGTCCACCAACCTCAC
CTGGTCCAGTGCCCTCCCTCCGGGCCAGGGGCCACAGCTCTGGCCGCTGCCCTGGGGAACCCACAGCTA
CAACATTACCCGCTCCTCAGGCCACGGAGTACTGGGCTGCCCTGCAAGTGGCCTTGTGATGCCACACCA
GTTGGCTTGTGATGGGCCAGGACCAAAGAGGCCACTCTTGTGCAAGAGCCTAGGGGATGTCCTGGCTCAT
TGCCATCCTGGCTCGCTGTGCTCTCCCTGGCAGCTGGCTAGGGCCACCTGGCACAGGCCAACCCAGGAA
GGGTGTGGGTGGAGGGCGGCTTCCAGCCTGGCTTCTGGGCTGGAGTGCCCTCTGTCGGGGTTGT
GTCTGCTCCCCCTCGTCTGCTGGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTTGCC
ACCATTGTCTCAAATTCTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTACAAA
AGAGAACAGACTGGGCCAGATGCCCTGCCAGGAAGGGACATGGACCCACGTGCTTGAGGCCTGGCAGCTGGC
CAAGACAGATGGGCTTTGTGGCCCTGGGGTGCTTCTGCAGCCTGAAAAAGTTGCCCTACCTCTAGGGTCA
CCTCTGCTGCCATTCTGAGGAACATCTCCAAGGAACAGGAGGGACTTGGCTAGAGCCTCTGCCCTCCCCATCTT
CTCTGCTGCCAGAGGCTCTGGGCCCTGGCTGCTCCCTACCTGTGTCCTGGGCTGCACCCCTCTCTTC
TCTTCTGTACAGTCTCAGTTGCTGCTCTGTGCTCTGGCAAGGGCTGAAGGGAGGCCACTCCATCTCAC
CTCGGGGGCTGCCCTCAATGTGGGAGTGACCCAGCCAGATCTGAAGGACATTGGGAGAGGGATGCCAGGAA
CGCCTCATCTCAGCAGCCTGGCTGGCATTCCGAAGCTGACTTTCTATAGGAATTGGTACCTTGTGGAGAA
ATGTGTCACCTCCCCAACCCGATTCACTCTTCTCTGTTGAAAAATAAAATAACAATAAAA
AAAA

FIGURE 86

MRLLVAPLLLAWVAGATATPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDNDLFLTA
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDSQNSFSDARDCDFHALPQQLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRSVLVAGMNLREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGLKFLDLNKNPLQRVPGDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHHLQPQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGDATKTVSVVVGALLQPGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVILLAAGLAAHLGTGQPRKGVGRRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGCCTGTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGAGGGGACATTGTGTACCGCCT
CTACATGCGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGCTACTACGTGCACAA
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCACCC
CCTGCCACACTCTCAAGATCCTGGCTCCTCTACATCAGCCTAGTCATCTCTACGGCCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCCTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCTCATGCTGCACCTCATTGACCAATACGACCCGCTACTCCAA
GCGCTTCGCCGTCTCTGCGGAGGTGAGTGAGAACAGCTGCGCAGCTGAACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGGGCTACCAAGAACCGCAGGACAAGCTGGAGCTGCACCTGTCATGCTCAGTGGCAT
CCCTGACACTGTGTTGACCTGGAGCTGGAGCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGC
CAGCATTGCCAGCTCACGGGCCTCAAGGAGCTGTCACACAGCGCCAAGATTGAAGCGCCTGCC
GGCCTTCTGCCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCGCTGTGGATCTA
TAGCCTGAAGACACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCCAGAACACCGCTACATGTCATCGA
CGGGCTGCCGGAGCTCAAACGCCCTCAAGGCTGCTGCCCTCAAGAGAACCTAAGCAAGCTGCCACAGGTGGTCA
AGATGTGGCGTGCACCTGCAGAACGCTGTCAGGAGCTGATCCGCTGCACCTGGAGCGCATCCCCACTCCATCTCAGCCT
CCACAACCTGAGGAGATTGACCTCAAGGACAACAACCTCAAGAACCATCGAGGAGATCATCAGCTTCCAGCACCT
GCACCGCCTCACCTGCCTTAAGCTGTTACAACCACATGCCCTACATCCCCATCCAGATCGCAACCTCACCAA
CCTGGAGCGCCTCTACCTGAACCGCAACAAGATCGAGAACGATCCCCACCCAGCTCTTCTACTGCCGAAGCTGCG
CTACCTGGACCTCAGCCACAACAACCTGACCTCCCTCCGACATCGGCTCTGCCAGAACCTCCAGAACCT
AGCCATCACGGCAACCGGATCGAGACGCTCCCTCCGGAGCTCTCCAGTGCAGGAAAGCTGCGGGCCCTGCACCT
GGGCAACAACGTGCTGCAGTCAGTCACTGCCCTCCAGGGTGGCGAGCTGACCAACCTGACGCAAGATCGAGCTGCC
CAACCGCTGGAGTGCCTGCTGGAGCTGGCGAGTGCCTCAAGCGCAGCGCTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCAGGTGAAGGAGCGCTGTGGAGGGCTGACAAGGAGCAGGCCCTGAGCGAG
GCCGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCAGGCCGGAGGGCAGGCCCTAGCTTCTCCAG
AACTCCGGACAGCCAGGACAGCCTCGCGCTGGCAGGAGCTGGGCGCTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGCTGGCCCTTTCTCCCTGAGACTCACGTCCCCAGGGCAAGTGCCTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTGATAATCAGGGCTCCTCCCTGGAGGCCAGCTCTGCCCAAGGGCTGAG
CTGCCACCAGAGGTCTGGACCCCTCACTTTAGTTCTGGTATTATTTCTCCATCTCCACCTCTTCATCC
AGATAACTTATACATTCCAAGAAAGTTCAGCCCAGATGGAAGGTGTTCAAGGAAAGGTGGCTGCCCTTTCCCC
TTGTCTTATTAGCGATGCCCGGGCATTAACACCCACCTGGACTTCAGCAGAGTGTCCGGGGCGAACCCAG
CCATGGGACGGTCACCCAGCAGTGCCTGGCTGGCTCTCGGGTCCACGGGAGAGCAGGCCCTCAGCTGGA
AAGGCCAGGCCGGAGCTGCTTCAGTTTGCGAGTTAGTTAGTTTTGTTTTTTTTTTAATCAA
AAACAATTTTTAAAAAAAGCTTGAATGGATGTTGGTATTAAAAAGAAAAAAACTAAAAAAA
AAAAGACACTAACGCCAGTGAGTTGGAGTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAAGGCCAGACGT
TGAACCTGTGTTCCCTTCCCTGGCGAGGGTGCAGGGTGTCTTCCGGATCTGGTGTGACCTTGGTCCAGGAGTT
CTATTTGTTCTGGGAGGGAGGTTTTGTTGTTGTTGGTTTTGGTTCTGGTGTCTTGTGTTCTTCTCC
ATGTGTCTGGCAGGCACTCATTCTGTGGCTGCGCCAGAGGGAAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTTGGTAATCCCCGGATGAAACGGTGCCTCCATTGCACCTCCCTCCTCGTGCCTGCCCTGCC
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTCGCCAGACTTTGTTCCCCACCTCTGCCAGGGTGTG
CCAGTGCACCGCTGCCCTCCGCTGCTTCCATCAGCCCTGCGCACCTGGCTCTCATGAAGAGCAGACACTTA
GAGGCTGGTGGGAATGGGAGGTGCCCCCTGGGAGGGCAGGGCTGGTTCCAAGGCCGGTCCCTGGCG
CTGGAGTGCACACAGGCCAGTCGGCACCTGGTGGCTGGAAGCCAACCTGCTTAGATCACTCGGGTCCCCACCTT
AGAAGGGTCCCCGCTTAGATCAATCAGTGGACACTAAGGCACGTTAGAGTCTTTGTCTTAATGATTATGT
CCATCCGTCTGCCGTCCATTGTGTTCTGCCGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGAAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAA
ATCTATAACAGAAAAAAA

FIGURE 88

MRQTI IKVIKFILII CYTVYYVHN IKFDV DCTVDIESLTGYRTYRC AHP LATLFK ILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESI REESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKL RQLNLN NEWTLDKL RQLTKNAQDKLELHLFMLSGIPD TVF DLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPAL AFLREN LRALHI KFTDIKEIPLWI
YSLKTLEELHLTGNL SAEENNRYIVIDGLRELKRLKVLRLKS NLSKLPQVVT DVGVHLQKLSI
NNEG TKLIVLNSLKKMANLTELELIRCDLERI PHSIFSLHNLQEIDLKDNNLKTIEE IISFQ
HLHRLTCLKLWYNHIA YIPIQIGNLTNLERLYLNRN KIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKL RALH LGNNV LQSLPSRVGE LTNL TQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFN TLPPEV KERLW RADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCCGCTGCTGGCCTGAACGCAGGAGCTGTCAATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCATACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGGC
CCCTTGACAGTGTCAAAACACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT
GTGGATAATCCCCTGGGACTGGGTTCAAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCATCAAGTGCACACTTGGGGGGT
TGCCTGGGTGATTCCCTGGATCTCCCTGTTGATTGGTGCCTCCTGGGGACCTTACCTGT
ACAGCATGTCCTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGGTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACTAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTACACAGAGGCCACCTAGTTGTCTTGTAGCGC
CACGTGAGACACCTACAACGAGATGCCCTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTAAAATTATTCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTAGGAGGCCTG
GGTGCAGAAACTGAAGTGGCCAGAACTGCCCTAAATTCAAGTCAGCTGAAGTGGAGGCCCTGT
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTCTGCTTCTAAAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTGCGCAGTCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGCCGTGGCA
GGGGAGCCTGCGCCTGTGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCGCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCACCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTACACTAAACACATCCAGCCATCTGTCTCCAG
GCCTCCACATTTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCCTCCAGGAAGTTCAGGTGCCATCATAAACAA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG
GTTTGTGCTGGCAACGCCAAGGCGGGAGGATGCCTGCTCGGTGACTCAGGTGGACCCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCCGGTGTACACCAATATCAGCCACCACCTTGAGTGGATCCAGAAG
CTGATGGCCCAAGAGTGGCATGTCCCAGCCAGACCCCTCCTGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTCTGTCTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAA

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

FIGURE 92

MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCVGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCGRPNRPGVYTNISHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACCGCGTCCGGACCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCCAGCCGACCAGCGAGGACGC
TGCCCCCAGGCTGGGTGCCCCCTGGCGTGCGGACCCCTGAGGAAGAGACTGAGTCACCTT
GCCCTGAGACAGCAGAATGTGGAAAGACTCTCGGAGCTGGCTGAGGCTGTGCGATCCCAG
CTCTCCTCAATACGGAAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGGCCATCCC
CACTGACCCCCACACGGTGCAGGGAAATGGCTTGGCAGCCGAGGCCAGAAGTGCATTCT
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTCATCACTATGTGGGAGGACCTACGGAAACCATGTTGTAAGGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCTTGGCCCCCATGTTGACTTGTGGGGGACTGCACCGT
TTTCCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGGTAACCCCTCTGTGATCCGTAAGCGATAACAACTTGACCTCACAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCTGGAGCAGTATTCCATGAC
TCAGACCTGGCTCAGTTCATGCGCTCTCGGTGGCAACTTGACATCAGGCATCAGTAGC
CCGTGTGGGGACAAACAGGCCGGGCCGGCCGGATTGAGGCCAGTCTAGATGTGAGT
ACCTGATGAGTGCTGGTGCACATCTCACCTGGGCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGGCCCTTCCTGCAGTGGCTATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGGCCCTACATCCAGGGTCA
ACACTGAGCTCATGAAGGCTGCCCTGGGTCTCACCTGCTCTCGCCTCAGGTGACAGT
GGGGCCGGGGTGTTGGCTGTCTCTGGAAAGACACCACTGCCCTACCTTCCCTGCCTCCAG
CCCCTATGTCACCACAGTGGAGGCACATCCTCCAGGAACCTTCCTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTCAGCAATGTTCCCACGGCCTTCATACCAGGAG
GAAGCTGTAACGAAGTTCTGAGCTAGCCCCCACCTGCCACCATCCAGTTACTCAATGC
CAGTGGCCGTGCCTACCCAGATGTTGCTGCACTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCCATTCCATGGGTGTCGGAACCTCGCCTCTACTCCAGTGTGTTGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTAGTGGCCGCCCCCTTGGCTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGCAGGTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGTAGAGGCCAGGGTTCTGCTCTGGCTGGCTGGATCCTGTAACAGGC
TGGGGAAACACCAACTCCCAGCTTGTAAGACTCTACTCAACCCCTGACCCCTTCTATC
AGGAGAGATGGCTTGTCCCCCTGCCCTGAAGCTGGCAGTTCAGTCCATTCTGCCCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
TGCTGTGAGCTTGACTTCACTCCAAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCTTAGATTCTCAATAAGATGCTGTAACTAGCATTTTGATGCTCTCCCTCCGC
ATCTCATCTTCTCTTCAATCAGGCTTCCAAAGGGTTGTATACAGACTCTGTGCAC
TTTCACTTGATATTCATTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGT
TTCCCTACCCGTACATCCAGAAACAATGGCCTCAGTGCATACTCTCAATCTTGT
GCCTTCCATCATAGTTGCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACTTCTG
ACTACTCTTGCTTCCCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTGC
TCCCAATTGATTTGCTCTCAGTTACTCATTGCTCCGGAAACAAATCACTGACA
TCTACAACCATTACCATCTCAACTAAATAAGACTTCTATCCAATAATGATTGATACCCTCAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSFTALRQQNVERLS
ELVQAVSDPSSPQYGKYLTL ENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLLPGAEFH YVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSDVGSCTSNNSQACAFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLM SAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHE SCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GGCGCGCGCTCTCTCCGGCGCCCACACCTGTCTGAGCGGCGAGCGAGCCGGCCGGC
GGGCTGCTCGCGCGGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTCCTTCTC
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATACCGCCTCCCTGCGTCTGCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCAGTGTCTAAGGGAAC
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAGGACTTCCTGCTCAACTACCCCTTCTAACATCAGTGAAGTT
ATCCACGGGCTGCACCGCACCCCTGGTGGCAGAGAACATGTCCCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAACGCTCGAGTGGCTTCTAAAGCCC
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCGAGCAGATGAA
ATTCAGTGGATCCGGGTGAAACGCACCCATGTGCCAAGGGTGGATCAAGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACTCAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGGTGAGCCCTCCTGCTAACGAGCTGCCAGGGGCCAGAACATTCACTTCTC
TGGTTATGACAATGACCGACCAGGAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTGCTCTACCAGCAATGCCATGCCAGCCAGGGGCCAGGGCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAACGAGGGGAAAAATTATTGGCATTTCAGG
GCACCAGTGGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG
TGACACAGTGTCCCTCCTGGCAGCAATTAGGGCTTCATGTTCTTATTTAGGAGAGGCC
AAATTGTTTGTCAATTGGCGTGCACACGTGTGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAAATG
GTTTGTGTATCATATCATATCATTAAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTGGGGCAATGAGGAATATTGACAATTAGTTAATCTCACGTTTG
CAAACTTGATTTATTCATCTGAACTTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRD
SGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVL
TAACIHDGKTYVKG
TQKLRVGFLKPKFKDGGRGANDSTS
AMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDV
KDETYDLYQQCD
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNV
AVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCAGCCCTGGGTGGGGCTGTCTCGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCAGGGTGTGGCGGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCAC TGCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCTGGCTCTGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCTGTGTATTCTGGAAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGCCTGCCATCTGCCTACCTGATGCCCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTCCCTTGC
CCCACCTCAGACCCCTGCAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTA CTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCCCTATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCAGCGAACAGGCC
GGGTCTACATCAGCCTCTGCGCACCGCTCTGGGTGGAGAAGATCGTCAAGGGTGCA
GCTCCCGGGCGCCTCAGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCG
CCGCGCGCTCCTAGGGCGCAGCGGACGCGGGCTCGGATCTGAAAGGCGCCAGATCCACA
TCTGGATCTGGATCTGCGGCGGCCTCGGCGGTTCCCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGCCAACGGCCTCATGTCCCCGCCCCAC
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTGTGTATATAATGTTAATGATTTTAT
AGGTATTTGTAACCCTGCCACATATCTTATTATTCCCTCCAATTCAATAATTATTATT
CTCCAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAHCFKDNLNKPYLF SVLLGAWQLGNPGSRSQKVGVVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGCCACCAATGCACGGCTCTGCAGTTCTGATGCTCTGCCGCTACTGCTA
CTGCTGGTGGCCACCAACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGCCCTCACAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCTTCGCCAAGGCCTACGCACGGCAGTGCAGTGGGGCCAC
AACAAAGGAGCGCGGGCGCCGGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGT
GCCGCTGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGGCCGCCACCT
GCAGCCCAGGCCAGATGTGCCGCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC
GGCTGTGGTCCCACCTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC
CGTGCTCCCAATGTCCCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTGCTTACCTGGTAACGTGAGGCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGGAAATGGGTACTCCTCTCCCTAGCAACGGGATTCCGGCTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC
CCAACTTCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCACCTGCGTAAC
AACTGAGGTCCCTTCCATTGGCAGCTCACAGCCTGCCCTCCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGGCCAGAGAACTCTGGACCCCAAGATGTCCCTGACAGGGCAAG
GGAACTCCTACCCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTCCAGTG
AGGTCTTGGCCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGTCTGCCAGGTGCAGAGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGCATGTGTGGGCCCTCCTGGGA
CTACTGCTCCTGCCTCCTGGTGTGGCTGGAATCTTCTTGAATGGGATACCAACTCAAAGGG
TGAAGAGGTCAAGCTGCTCCTGTCACTTCCCCACCCCTGTCCCCAGCCCTAAACAAGATA
CTTCTGGTTAAGGCCCTCCGAAGGGAAAGGCTACGGGCATGTGCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCTCCCTGCCCTCCCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT
CACTGCCTACCTGGCCTGGGCTGTCGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG
TGTAGCTGGGGATGGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTC
TTTGAGTGGGGAGGCAGGGACGAGGAAGTAACCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGETPCSQC
PSGYHCKNSLCEPIGSPEADAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEALPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVWGPLLGLLLPPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACGTGAGTCAGGCTTTCATTTGGGAAGCCCCCTCAACAGAACGAGTCATTCTCCAAGTTATGGTGGACGT
ACTTCTGTTCTCCCTCTGCTTACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTCAT
CAAGGCAAGTCCATGAGCCACCTTCAAAGCCTCGAGAAGTGAACACTGAACAACAAATGAATTGGAGACCATTCC
AAATCTGGGACCAAGTCTCGGCAAATATTACACTTCTCTCCGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
ACATCTGAAAGAGTTTCAGTCCCTGAAACTTGGACCTAGCAGCAACAATATTCAGAGCTCCAAACTGCATT
TCCAGCCCTACAGCTCAAATATCTGTATCTAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTGACAA
TTTGGCCAACACACTCCTGTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTAAACT
GCCCAACTGCAACATCTGAATTGAACCGAAAGATTAAAATGTAGATGGACTGACATTCCAAGGCCTGG
TGCTCTGAAAGTCTGAAATGCAAGAACGAAATGGAGTAACGAAACTATGGATGGAGCTTTGGGGCTGAGCAA
CATGAAATTTGCACTGGACCATAACAACTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGCTGATGCT
GCAGGAACCTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTCTGCCAGAAGCTCAG
TGAGCTGGACCTAACTTCAACTACATTCAAGGTTAGATGATTCAAGCTCCTGGCCAAGCTTACTAAATAC
ACTGCACATTTGGAACAAACAGACTCAGCTACATTGCTGATTGCTCTCCGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAAGAACAAATGAAATTCCCTGGACTATTGAAGACATGAATGGTGTCTCTGGGCTTGACAAACTGAG
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTACTGGTTGGATGCAATTGGAGCA
TCTAGACCTGAGTGACAAACGAATCATGTTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAAATT
GCATTAAATACATCAAGCCTTGTGGATTGCCAGCTAAATGGCTCCACAGTGGTGGGGAAAACAACTT
TCAGAGCTTGTAAATGCCAGTTGTGCCCCATCCTCAGCTCTAAAGGAAGAACGATTGGCTGTTAGCCCAGA
TGGCTTGTGTGATGATTCCAAACCCAGATCACGGTCAGCCAGAACACAGTCGGCAATAAAAGGTT
CAATTGAGTTCATCTGCTCAGTGCAGCAGCAGTGATTCCCAATGACTTTGCTTGGAAAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCAAGGTTGGCGAGGTGATGGAGTATACCAC
CATCCTCGGCTGCGCAGGTGGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCCAATCACTTGGTT
ATCCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACC
CCGAGCTGGGGCATGGCACGCTGGAGTGCTGCTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA
TGGGGCACAGACTTCCAGCTGCACGGAGAGACGATGCATGATGATGCCAGGATGACGTGTTTATCGT
GGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTGCAAATGC
AACTCTGACTGTCCTAGAAACACCATCATTTCGGCCACTGTTGGACCGAATGTAACCAAGGGAGAAACAGC
CGTCCCTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACCTGGACCAAAGATGATAGCCCATTGGTGG
AACCGAGAGGCACTTTTGCACTGCAGGCAATCAGCTCTGATTATTGTGACTCAGATGTCAGTGTGCTGGAA
ATACACATGTGAGATGTCACACCCCTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAAC
CTGCGACTCCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGC
CGTGGTTGCTGTGGGGCACGTCACTCGTGTGGGTGTCATCATATACACACAAAGGCGGAGGAATGAAGA
TTGCAGCATTACCAACACAGATGAGACCAACTTGCAGCAGAGTATTCTCTAGTTATTGTCATCTCAGGGAAACTT
AGCTGACAGGCAAGATGGGTACGTGCTTCAGAAAGTGAAGGCCACCCAGTTGTCACATCTCAGGTGCTGG
ATTTTCTTACACAAACATGACAGTAGGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAAAGCTGC
CACAGATCTGTCCTTGTCCGTTTGGGATCCACAGGCCCTATGTATTGAAAGGGAAATGTGATGGCTCAGA
TCCTTTGAAACATATCATACAGGTTGCAGTCTGACCCAAAGAACAGTTTAATGGACCAACTATGAGCCCAGTT
CATAAAGAAAAGGAGTGCCTACCCATGTTCTCAGAACATCCTGCGAACGGAGCTCAGTAATATATC
GTGGCCTTCACATGTGAGGAAGCTACTAACACTAGTTACTCTCACAAATGAAGGACCTGGAATGAAAATCTGTG
TCTAAACAAGTCTCTTGTGAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGT
TACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGT
AAGAGCCTTTATTGAAAGCTCATCTTCCCCAGACTTGGACTCTGGGTAGAGGAAGATGGAAAGAAAGGAC
AGATTTCAGGAAGAAAATCACATTGTACCTTAAACAGACTTTAGAAAATACAGGACTCCAAATTTCAGTC
TTATGACTTGGACACATAGACTGAATGAGACCAAGGAAAAGCTTAACATACACTACCTCAAGTGAACCTTATT
AAAGAGAGAGAATCTTATGTTTAAATGGAGTTATGAATTAAAAGGATAAAATGCTTTATTACAGAT
GAACCAAATTACAAAAAGTTATGAAAATTTCAGTGGAAATGATATACTGATTATTTATGTATT
TTATAATGCCAGATTCTTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCATTGACCAATT
TTAAATAGAAGTTACTCATTATATTGCACTTATTTAATAAAATGTGCAATTGAA

FIGURE 102

MVDVLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQLSLREVKLNNNELETIPNLGPVSA
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNISAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMGAFWGGLSNMEILQLDHNNLTEITKGWLGYLLMLQELHLSQNAIRISPD
FCQKLSLELDLTFNHLRLDDSSFLGLSLLNLTIGHNNRVSYIADCAFRLSSLKTL
LKNNEISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNA
IMSLQGNAFSQMKKLQQLHLNTSSLLCDCQLKWLQPQWVAENNQSFVN
ASCAHPQLLKGRSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSF
ICSAASSSDSPMTFAWKKDNE
LLHDAEMENYAHLRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSY
SVAKLT
VNMLPSFTKTPMDLT
IRAGAMARLECAAVGHPAPQIAWQKDGGTDFPAARERRM
HVMPEDDVFFIVDV
KIEDIGVY
SCTAQNSAGSISANATLT
VLETPSFLRPLL
DRVT
KGETAVLQCIAGG
SPPP
KLNWT
KDD
SPLV
VTERHFFAAGNQLL
IIVDS
DVSDAG
KYTC
EMSN
TLG
TERGN
VRL
SVI
PT
PTC
DSP
QMT
APS
LDD
DG
WATVG
VII
IAVV
CCV
VGT
SLV
WV
VII
IYH
TR
RR
NED
CS
IT
NT
DE
TN
LP
AD
I
PSY
LSS
QGT
LAD
RQDG
YVS
SE
SGSH
HQF
V
TSS
GAG
FFLP
QHD
SSGT
CHID
NS
SE
AD
VE
A
AT
DL
FL
CP
FLG
STGP
MYLK
GNV
Y
GSD
PF
TY
HT
GC
PD
P
RT
V
L
MD
H
YE
PSY
IK
K
KE
C
Y
PC
S
HP
SE
E
SC
E
RS
FS
N
I
SW
PSH
VR
K
L
L
NT
SY
SH
NE
PG
MK
NL
CL
NK
SS
LDF
S
AN
PE
P
A
S
V
A
S
NS
FM
GT
FG
K
A
L
R
R
P
H
L
D
A
Y
SS
FG
Q
P
S
DC
Q
P
R
A
F
Y
L
K
A
H
S
P
D
L
S
G
SE
E
D
G
K
E
R
T
D
F
Q
E
E
N
H
I
C
T
F
K
Q
T
L
E
N
Y
R
T
P
N
F
Q
S
Y
D
L
D
T

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459, 628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268, 314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653, 671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962, 1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534, 612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGAAAAGGAGACTTTTTGGTGGTGGCTGGTGGGTGCCTGCAAAATG
AAGGATGCAGGACGCAGCTTCTCTGGAACCGAACGCAATGGATAAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
TAAACCAGAGTTAGACCCGCGGGGTTGGTGTGTTCTGACATAAAATAATCTAAAGCAGCTGTTCCCCCTCC
CCACCCCCAAAAAAAGGATGATTGGAATGAAGAACCGAGGATTACAAAGAAAAAGTATGTTATTTC
TATAAAGGAGAAAGTGAGCCAAGGAGATATTGGAAATGAAAAGTTGGGCTTTTAGTAAAGTAAGAAC
GGTGTGGTGGTGTCTTCTTCTTGAATTCCACAAGAGGGAGGAAATTAAATAACATCTGCAAGAGAAA
TTTCAGAGAAGAAAAGTTGACCGCGGAGATTGAGGATTGAGGATTGAGGAGAGAAACCAGCAGAGCACAGTTGGA
TTTGCGCTATGACTAAATTGACGGATAATTGCAAGTGGATTTCATCAACCTCCTTTTTAAAT
TTTATTCTTCTTGTATCAAGATCATGCGTTCTCTGTCTTAAACCACCTGGATTTCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACACTGTTGAATTCCAGAACGGACAAACACCAGATAAAATTATGAATGTTGAACAAGAT
GACCTTACATCCACAGCAGATAATGAGGTTAACAGGGCCATTGACCCCTGCTGTGGCT
GCTGGCTCTTCAACTCTGTGGTGGCTGGTCTGGCGGGCTCAGACCTGCCCTCTGTGCTCCTGAGCAA
CCAGTTCAAGGTGATTGTGTTGGAAACAAATCCAGATCATCAAAGTGAACAGCTCAAGCACTTGAGGCACTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCATGGAAATTGGGCTTCAATGGTCTGGCGAACCTCAACACTCTGGA
ACTCTTGACATCGTCTACTACCATCCGAATGGAGCTTTGTATACTTGTCTAAACTGAAGGAGCTCTGTT
GCGAAACAACCCATTGAAGCATCCCTCTTATGCTTTAACAGAATTCCCTTTGCGCGACTAGACTTAGG
GGAATTGAAAAGACTTCATACATCTCAGAAGGTGCCCTTGAAGGTCTGTCAAATTGAGGTATTGAAACCTTGC
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAAGTGAACAGCTGAGGATCTTCTGGGAAATCA
TTTATCTGCCATCAGGCCCTGGCTTTCCAGGGTTGATGCACCTCAAAACTGTGGATGATACTGCCCAGAT
TCAAGTGATTGAACGGAATGCCCTTGACAACCTCAGTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC
ATTACTGCCTCATGACCTTCACTCCCTGATCATCTAGAGCGGATACATTACATCACACCCCTTGGAACTG
TAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTGAACACAGCTTGTGCCCCGGT
TAACACTCCTCCAATCTAAAGGGAGGTACATTGGAGAGCTGACCAGAATTACTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGAGACCTCAATGTCAGTCAAGGCATGGCAGCTGAGCTGAAATGTCGGCCTCCACATC
CCTGACATCTGATCTGGATTACTCCAAATGGAACAGTCAGTCAGACACATGGGGCTACAAAGTGCAGGATAGCTGT
GCTCAGTGTGATGGTACGTTAAATTTCACAAATGTAACGTGCAAGATACAGGCATGTACACATGTATGGTGGTAA
TTCCGGTGGGAAATACTACTGTGCTTCAGCCACCTGAATGTTACTGCAAGCAACCAACTACTCTTCTTCTT
AACCGTCACAGTAGAGACTATGGAACCGCTCAGGATGAGGACGGGACACAGATAACAATGTCGGTCCCACCTCC
AGTGGTCGACTGGGAGACCAACTGTGACCCCTCTCACACCAAGAGCACAAGGGTCGACAGAGAAAACCTT
CACCATCCCAGTGACTGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCTGAAGACTACCAAAATCATCAT
TGGGTGTTTGTGGCATCACACTCATGGCTGAGTGTGCTGGTCTTACAAGATGAGGAAAGCAGCACCA
TCGGAAAACCATCACGCCAACAGGACTGTTGAAATTATTAATGAGGATGAGGATTAACGGGAGACACACC
CATGGAAAGCCACCTGCCATGCCTGCTATCGAGCATGAGCACCTAAATCAACTATAACTCATACAATCTCCCTT
CAACCCACACAACAGTTAACACAATAATTCAATACACAGTTCACTGCATGAACCGTATTGATCGAATGAA
CTCTAAAGACAATGTACAAGAGACTAAATCTAAACATTACAGAGTTACAAAAAAACAAACATCAAAAAAA
GACAGTTATTAAAAATGACACAAATGACTGGCTAAATCTACTGTTCAAAAAAGTGTCTTACAAAAAAACAA
AAAAGAAAAGAAATTATTATTAAACATTCTATTGTGATCTAAAGCAGACAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHHNPWCNC
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLN
TEGMAAE LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTN
TVQDTGMYTCMVSNSVGN TTASATLNVTAATTPFSYFSTVT
VETMEPSQDEARTTDNNVGPTVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINS
GIPGIDEVMKTTKIIIGCFV
AITLMAAVMLVIFYKMRKQHHRQ
HHAPTRTVEIINV
DDEITGDT
PMESHPMP
AIEHEHLN
HYNSYKSP
FNHTTVNT
INSIHSS
VHEPLL
IIRMNS
KDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTCAGTTGGCAGTTCTTCCCTCTGCTTTGGGGCA
TGAAAGGGCTTCGCCCGGGAGTAAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCGCACCGC
GAGGGCGGGCGTGCACCCCTCGCTGGAGTTGTGCCGGGCCCCAGCGCGCCGGCTGGAGCTGGTAGA
GACCTAGGCCGCTGGACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCCGGTGGGGTAGCTGTGC
GCGGTCTGGGCGCGCTGGCCGACAGCGGGCGGGACTCGGGCAGCCCTCTGGGTAGCCGCC
GAGCGCCCATGCCCACTACCTGCCGCTGCCCTGGGACCTGACTGCACTGTAAGCGGCTAGCGCTCTT
CCCAGGCACTCCGCTCTGGCTCGGACTTAAGTCACAACAGATTATCTTCATCAAGGCAAGTTCC
ATGAGCCACCTTCAAAGCTCGAGAAGTGAACACTGAAACAACAATGAATTGGAGACCAATTCAAATCTGGACCA
GTCTCGGAAATATTACACTTCTCTTGGCTGAAACAGGATTGTGAAATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCCTTGAACATTGGACCTTAGCAGCAACAAATATTCAAGAGCTCCAAACTGCAATTCCAGCCCTACAG
CTCAAATATCTGTATCTAACAGCAACCGAGTCACATCAATGGAAACCTGGTATTGACAATTGGCAACACAA
CTCCTGTGTTAAAGTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTAAACTGCCCCACTGCAA
CATCTGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCTTGGTGCCTGAAGTCT
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGCTGAGCAACATGGAAATTGG
CAGCTGGACCATAACAAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGCTGATGCTGCAGGAACCTCAT
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCTGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
ACTTCATCAACTTATCAAGGTTAGATGATTCAAGCTTCTGGCCTAAGCTTACTAAATAACACTGCACATTGG
AAACAACAGAGTCAGCTACATTGCTGATTGTGCCCTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAAGAAC
AATGAAATTCTCTGGACTATTGAAGACATGAATGGTCTTCTCTGGGCTGACAAACTGAGGCAGTGATACTC
CAAGGAAATCGGATCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCATTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGTCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAATTGCAATTAAATACA
TCAAGCCTTTGTGCAGCTAAATGGCTCCCACAGTGGTGGCGAAAACAACCTTCAGAGCTTGT
AATGCCAGTTGTGCCCATCCTCAGCTGCTAAAGGAAGAACGATTGGTCTAGCCAGATGGCTTGT
GATGATTTCCTAAACCCAGATCACGGTTAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTGAGTT
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTGCTTGGAAAAAGACAATGAACACTGCTGATGAT
GCTGAAATGGAAAATTATGCACACCTCGGGGCCAAGGTGGCGAGGTGATGGAGTATACCACCATCCTCGGCTG
CGCAGGTGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCCAATCACTTGGTCTACTCTACTCTGTC
AAAGCCAAGCTTACAGTAAATATGCTTCCCTATTCCAAGACCCCCATGGATCTCACCATCCGAGCTGGGCC
ATGGCACGCTGGAGTGCTGCTGCTGGGCCACGGCCACCCAGATAGCTGGCAGAAGGATGGGGCACAGAC
TTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCAGGATGAGCTGTTCTTATCGGGATGTGAAGATA
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTCAGCAAATGCAACTCTGACTGTC
CTAGAAACACCATCATTTCGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAACAGCCGTCCTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAAGATGATGCCATTGGTGGTAACCGAGAGGCAC
TTTTTGCAGCAGGCAATCAGCTCTGATTATTGTGGACTCAGATGTCAGTGCTGGAAATAACATGTGAG
ATGTCTAACACCCCTGGCACTGAGAGAGGAAACGTGCCCTCAGTGTGATCCCCACTCCAACCTGCCACTCCCT
CAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGCTGATCATAGCCGTGGTTGCTGT
GTGGGGCACGTCACTCGTGTGGGTGTCATCATATACCACACAAGCGGAGGAATGAAGATTGCAAGCATTAC
AACACAGATGAGACCAACTGCCAGCAGATATTCTTAGTTATGTGTCATCTCAGGGAACGTTAGCTGACAGGAG
GATGGGTACGTGCTTCAGAAAGTGGAGCCACCAAGCTTGTACATCTCAGGTGCTGGATTTTCTTACCA
CAACATGACAGTAGTGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGGAAGCTGCCACAGATCTGTC
CTTTGTCGTTTGGATCCACAGGCCCTATGTATTGAAGGGAAATGTGTATGGCTCAGATCCTTGAACAA
TATCATAACAGGTTGCACTGCCAGCAGATATTCTTAGTTATGTGTCATCTCAGGGAACGTTAGCTGACAGGAG
GAGTGCACCCATGTCATCTCAGAAAGAATCTCGCAACGGAGCTTCAGTAATATATCGTGGCTTCACAT
GTGAGGAAGCTACTTAAACACTAGTTACTCTCAGAAGGACCTGGATGAAAATCTGTCATCAAAGTCC
TCTTAGTTTGTGCAATCCAGAGGCCAGCGTCGGTGCCTCGAGTAATTCTTCATGGTACCTTGGAAAA
GCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTGGACGCCATCAGATTGTCAGCCAAGAGCCTTGT
TTGAAAGCTCATTCTCCCCAGACTGGACTCTGGGTCAAGAGGAATGGGAAAGAAAGACAGATTTCAGGAA
GAAAATCACATTGTACCTTAAACAGACTTAGAAAACAGCTTAACACTACCTCAAGTGAACCTTTTATTTAAAGAGAG
ACATAGACTGAATGAGACCAAGGAAAGCTTAACACTACCTCAAGTGAACCTTTTATTTAAAGAGAG
CTTATGTTTTAAATGGAGTTATGAATTAAAAGGATAAAAATGCTTATTATACAGATGAACCAAATTAC
AAAAAGTTATGAAATTTTATACGGGAATGATGCTCATATAAGAATACCTTTAAACTATTTTAACTTAACTT
TTTATGCAAAAAGTATCTACGTAATTAAATGATATAATCATGATTATTGTATTGTTATAATGCCAGA
TTCTTTTATGGAAAATGAGTTACTAAAGCATTTAAATAACCTGCCCTGTACCATTTTAAATAGAAGTT
ACTCATTATATTGCACTTAAATAATGTCATTGAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQLSREVKLNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRIASAIPPKMFKLPQLQHLELNRNKIKNVGGLTFQGLGALKSLKMQR
NGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC
QKLSELDLTFNHLSRLDDSSFLGLSLLNLTIGHNNRVSYIADCAFRLGSSLKTLDLKNEIS
WTIEDMNGAFSGLDKLRRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQQLHLNTSSLLCDCQLKWLPOVVAENNFQSFVNASCAPQLLKGRSIFAVSPDGFVCDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRVTKGETAVLQCIAGGSPPPKNWTKDDSPVVTERHF
FAAGNQLLIIVDSDVSDAGKYTCMSNTLGTTERGNVRLSVIPTPTCDSPQMTAPSLLDDGWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLD
Signal sequence:
amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGCGGAGAGCGCCAGCTGACTTGAATGGAAGGAGCCCGAGCCCGGGAGCGCAGCTGAGAC
TGGGGGAGCGCGTTCGGCCTGTGGGGCGCCGCTGGCGCCGGGGCGCAGCAGGGAGGGGAAGCTGTGGTCTGCC
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCCTGGTGGTCCCGTCCCCTATCCCTCTTTATATA
GAAACCTTCCACACTGGGAAGGCAGCGGAGGCAGGAGGGCTATGGTGAGCAAGGAGGCCGCTGATCTGAG
GCGCACAGCATTGGAGTTACAGATTTACAGATACCAATGGAAAGGCAGGAGGCAGAACAGCCTGCCCTGGT
TCCATCAGCCCTGGCGCCAGGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCAGAGGCCGGTGTG
TGCTCCTGCTGCTGCTGCCACAGCTGCACCTGGGACCTGTGCTTGCGTGGAGGAGGCCAGGATTGGCCGAA
GTGGCGGCCACAGCTGAGCCCCGAAGAGAACGAATTGCGGAGGAGGCCGTGCTGTTACTGAGCCCTGAGG
AGCCCCGGCTGGCCAGCCGCGTCAAGCTGCCCGAGACTGTGCTGTTCCAGGAGGGCGTGTGACTGTG
GCGGTATTGACCTGCGTGAGTCCCGGGGACCTGCGCTGAGCACACCAACCAACTATCTGAGAACAAAC
TGGAAAAGATCTACCCCTGAGGAGCTCCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAAACAAAC
CTTCCCAGGGCTCCAGAGAACGGCTTGGACATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC
TGACCTGGCACCCGCTCTGACAAACGCCCTGATCAGTGTGACTTGTGCGCAACTATCTCACCAAGATCT
ATGGGCTCACCTTGGCCAAGGCAAACCTGAGGTCTGTGACTTGCAACAAACAGCTGGCAGACGCCGGC
TGCGGACAAACATGTCACAGGCTCAGCAACGTCGAGGTCTCATCTGTCCAGCAACTTCCCTGCGCCACGTG
CCAAGCACCTGCCGCTGCCCTGTACAAGCTGCACCTCAAGAACACAAGCTGGAGAAGATCCCCGGGGC
TCAGCGAGCTGAGCAGCTGCGAGCTATACTGCAGAACAACTACCTGACTGACGAGGGCTGGACAACGAGA
CCTCTGGAAGCTCTCAGCCTGGAGTACCTGGATCTGTCAGCAACAACCTGTCTCGGGTCCCAGCTGGCTG
CGCGCAGCCTGGTGTGTCACCTGGAGAAGAACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCATCC
GCAGCCTGGAGTACCTGCTGTCACAGCAACCAGCTGCCAGGGCATCCACCCACTGGCCTCCAGGGC
TCAAGCGGTTGACACGGTGCACCTGTACAACAACAGCGCTGGAGGCCGTGCCAGTGGCCTGCCCGTGC
GCACCCCATGATCCTGACAAACAGATCACAGGCACTGGCGGAAGACTTGGCACCACCTACTTCTGGAGG
AGCTAACCTCAGCTACAACCGCATCACCAGCCACAGGTGACCGCCTCCGCAAGCTGCCCTGCTG
GCTCGCTGGACCTGTGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCAGTGGACATTGCTGCTG
TCAAGCGCAATGAGCTGGCTGCCCTGGCACAGAGGGCGCTGGCGGATGGCTCAGCTGGTGTAGCT
CCAGCAACCGACTGCGCAGCCCTGGGCCCCGTGCCTGGTGGACCTGCCCATCTGAGCTGCTGGACA
TCGCCGGAAATCAGCTCACAGAGATCCCCGAGGGCTCCCGAGTCACTTGAGTACCTGACAGAACACA
AGATTAGTGCGGTGCCGCAATGCCCTCGACTCCACGCCAACCTCAAGGGATCTTCTCAGGTTAACAGC
TGGCTGTGGCTCCGTGGACAGTGCCTCCGGAGGTGAAGCACCTGCAGGTCTTGAGCATTGAGGCAACT
TAGAGTTGGTGAATTTCAAGGACCGTGGCGCTTGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGGAG
AGGAAGAGGAAACAAGATAGTGCACAGGTGATGCAGATGTGACCTAGGATGATGGACGCCGACTCTTCTG
AGCACACGCCCTGTGTGACTGCCCTCCGACACAGCTCATATCCCCACCCCTCCACGGCGTGTCCCAGG
TCCCACATGACACGGCTGACACAGTCTCATATCCCCACCCCTCCACGGCGTGTCCCAGGACACATGC
ACACACATCACACCCCTCAAAACACCCAGCTCAGCCACACACAACACTACCCCTCAAACACAGTCT
GTGACACCCCCACTACCGCTGCCACCCCTCTGAATCATGCAGGGAGGGCTGCCCTGCCACACACAGG
CCCCCTACCGCTGCCACCCCTCTGAATCATGCAGGGAGGGCTGCCCTGCCACACACAGGACCA
TTCCCTCCCCCTGCTGACATGTGATGCGTATGCAACACACACACACATGCAAGTCATGTGCGAA
CAGCCCTCCAAGCTATGCCACAGACAGCTCTGCCAGCCAGAACATGCCATAGCAGCTGCCGCTGCC
GTCCCATCTGTCGTCCGTTCCCTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCG
GGAACTCACAAAAGCTGGTTTATCCTTCCATCCTATGGGGACAGGAGGCCCTCAGGACTGCTGGC
TGGCCCACCCCTGCTCCCTCAGGTGCTGGGAGTCACCTGCTAAGAGTCCCTCCCTGCCACGCC
CAGGCACTTTCAATGGCAAGCCAGTGGAGGAGGATGGAGAGGCCCTGGGTGCTGCTGGG
CAGGAGTGAAGCAGAGGTGATGGGCTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCAC
CTAGGAGACACCTTGTCTTCTGTTATAGAAAACATAAAGCATTATCCCTATGCC
CTCAAAGCTGATTTCTGTTATAGAAAACATAAAGCATTATCCCTATGCC
CTGCAAAAAAA

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENEFAEEEPVLVLSPEEPGP GPAVSCP RD CACS QEGV VDCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKA FEHLTNLYLYLANNK
LT LAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPA GLPRSLVLLHLEKNAIRSDANVLTPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLP RRVRTLMILHNQITGIGREDFATTYF
LEELNLSYNRITS PQVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSA FRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCGCGCCTGCCGCTGCTCTCCGGGAGCGGCAG
CACTAGCCCAGGGCGGCGAGGGCTGGGGCTCTCGAGACTCTCAGAGGGCGCCTCCCATGGCGCCACCACCC
CAACCTGTTCTCGCGCCACTGCGCTGCCAGGACCCGCTGCCAACATGGATTCTCTGGCTGGT
GCTGGTATCCTCGCTCTACCTCGAGGCGGCCAGTTCGACGGGAGGTGGCCAGGAAATAGTGTATCGAT
TGGCCTATGCGTTATGGTGGAGGATTGACTGCTGCTGGGCTGGCTGCCAGTCTGGGACAGTGTAGCC
TGTGTGCCAACACAGATGCAAACATGGTGAATGTATCGGGCAAACAAGTCAAGTGTATCCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGCCCCGGCCCTGTAAGCACAGGTGATGAACACTTA
CGGCAGCTACAAGTGTACTGTCTCAACGGATATATGCTCATGCCAGTGGTCTGCTCAAGTGCCCTGACTG
CTCCATGGCAAACGTCACTATGGCTGTGATTTAAAGGACAAATACGGTGCAGTGCCAGTGCCATCCCTGGCCT
GCACCTGGCTCTGATGGGAGGACCTGTGATGGTGAATGTGCTACAGGAAGGACCTGGCTGCCCTAGATT
TAGGCAATGTGTCACACTTTGGGAGCTACATCTGCAAGTGTCACTGGTCAAGTGTGCTACAGGCTTCGATCTCATGTATATTGGAGG
CAAATATCAATGTCAAGACATAGACGAATGCTCACTGGTCAAGTGTGCTACAGGCTTCGATGTGCTGATGTATAA
CGTACGTGGGCTCTACAAGTGCAGGAAATGTAAGGAGGATACAGGGTGAATGGACTGACTTGTGATATCCCCAA
AGTTATGATTGAACCTCAGGTCCAATTGATGTTACCAAAAGGAAATGGTACCTTAAAGGGTACACAGGAA
TAATAATTGGATTCCCTGATGGTGGAAAGTACTTGGTGGCTCCGAAGACACCATATATTCCCTATCATTACCAA
CAGGCCTACTTCAAGCCAACAAGACCTACACCAAGCCAACACCAATTCTACTCCACCACACCACCC
CCTGCCAACAGAGCTCAGAACACCTCTACCCACTACAACCCAGAAAGGCCAACACCAGGACTGACAACATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGACGCCCTGAGAAACCCAGGG
AGATGTGTTAGTGTCTGGTACACAGTTGTAATTTGACCATGGACTTTGGATGGATGGATCAGGGAGAAAGACAA
TGACTTGCAGTGGAAACCAATCAGGGACCCAGCAGGTGAGCAATATCTGACAGTGTGGCAGGCCAACGCCCCAGG
GGGAAAAGCTGCACGCTTGGTGTACCTCTGGCCCTCATGCATTCAAGGGACCTGTGCTGTGATTCAAGG
CAAGGTGACGGGCTGCACTCTGGCACACTCCAGGTGTTGTGAGAAAACACGGTGCCACGGAGCAGCCCTGTG
GGGAAGAAATGGTGGCCATGGTGGAGGCAAACACAGATCACCTTGCAGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAGGGTTGGAAAAAAAGATCTATGAGGGAAATTAAAGGAACGGTATTGAGCCTGGAGAAG
AGAAGACTGAGGGCAAACCATGATGGTTCAAGTATATGAAGGGTGGCACAGAGAGGGTGGCACCAGCTG
TTCTCCATATGCACTAAGAATAGAACAGAGGAAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTGGCAGG
GGCATTGTTAGAATACTCATAAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTTCTAAAAAATTAGA
TAAAAATTGCTATTAAGATGGTAAAGATGTTCTACCAAGGAAAGTACAAATTATAGAATTCCCAA
AGATGTTTGATCCTACTAGTAGTATGCACTGAAAATCTTACAATTAAATTGGACAAGGCTTAATTAGG
CATTCCTCTTGACCTCTAAATGGAGAGGGATTGAAAGGGGAAAGAGGCCACAAATGCTGAGCTCACTGAAATA
TCTCTCCCTATGGCAATCCTAGCAGTATTAAGAAAAAAGGAAACTATTTATCCAAATGAGAGTATGATGGAC
AGATATTAGTATCTCAGTAATGTCCTAGTGTGGCGGGTTTCAATGTTCTCATGGTAAAGGTATAAGCC
TTTCATTTGTTCAATGGATGATGTTCAAGATTTTTTTTAAGAGATCCTCAAGGAACACAGTTCAAGGAG
ATTTCATGGGTGCATTCTCTGCTTGTGTGACAAGTTATCTGGCTGCTGAGAAAAGAGTGCCCTGCC
ACACCGCAGACCTTCTCACCTCATCAGTATGATTGAGTTCTGTCATTAAACCTGGTAAAGGCAGGGCTGG
AGGGGAAAATAATCATTAAGCCTTGAGTAACGGCAGAAATATGGCTGAGTCCATTAAATGGTTCA
TCCTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGAAAATAATGAAAATTACTTTGATGCCAA
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTATTATTAATGTTT
CTAAAATAAAAATGTTAGTGGTTTCCAAATGGCCTAATAAAAACAATTATGTAAATAAAACACTGTTACTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGE CIGPNKCKCHPGYAGKTCNCQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGC DVVKGQIRCQCPSPGLHLAPDGRTCDVDECATGRASCPRFRC
VNTFGSYICKCHKGFDLMIYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTT PERPTTGLTTIAPA AASTPPGGITVDN
RVQTDPQKPRGDVFSLVHSCNFDHGLCGWIREKDNDLHWEPIRD PAGGQYLTVSAAKAPGG
KAARLVLPLGRLMHSGLC LSF RHKV TLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACCTTCCTTCCTTGCAACAGGTGCTGCTGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCA
CACAAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTGACTTGAATACC
AACACAAGTTACCATGATGCCACCCAATGCATCTGCTTATCAACCCACTGCAGTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAAGGAAATGGAACACTATCTGCCAGTCA
GAAGATAACAAGTCACGGTTGATGATCCTGTACAAAGCCAGTGGTGCAGATTCACTCCCT
CTGGGGCTGGAGTATGTGGGGACATGACCTGACATGCCATGTGGAAGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTC
TCCCCAAACAATACCCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGAATTACAGCT
GCCTGGTGAGGAACCCCTGTCAGTGAATCTGATAAAGGGCTAAAGTAGGGGAAGTGTACTGT
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAAGCATGGGCCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCAGAACAGACAATGGACTATGTGTGCTTACAACAAACATAAC
CGGCAGGCAAGATGAAACTCATTACAGTTATCATCACTCCGTAGGACTGGAGAAGCTG
CACAGAAAGGAAAATCATTGTCACCTTAGCAAGTATAACTGGAATATCACTATTTGATT
ATATCCATGTGCTTCTCTTCTATGAAAAAAATCAACCCCTACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAACAGAACAGAACAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATATGAATTGTTGCTTCCAGATGTTCTGGTGTTCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATGGGGCAAGATTGCACAGTACAGT
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATTCAAGAGT**GTAA**CTTCATGG
GCTAAACAGTACATTGAGTGAAAATTCTGAAGAAACATTAAAGGAAAACAGTGGAAAAGT
ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTACTCATTATCCTTACA
TGCAGAACAGGGCATTTATGCAAATTGAACACTGCAGGTTTCAGCATATAACAAATGTCTT
GTGCAACAGAAAACATGTTGGGAAATATTCCCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGGTTCCCTCATAAGTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAAACTTACATTGTTGATTTTCAGCAGACTTGTGTTATTAAATTGTTATTAGTG
TTAAGAATGCTAAATTATGTTCAATTATTCCAAATTCTATCTGTTATTGTACAA
CAAAGTAATAAGGATGGTTGTCAACAAAACAAAACATGCCTCTCTTTTTCAATCACC
AGTAGTATTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA
TTTTTTCAAGGAAAGATGGATTCAAATAATTATTCTGTTTGCTTTAAAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGTLSASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMVDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGSRIPSRSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTGCAGTTCCCCTGGCAGTCCTGGTGCTGTT
GCTTGGGGTGCTCCTGGACGCACGGCGGGAGCAACGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAAGGAGACTGGATGATAGAATTTATGCCCCGTGGTGCCCTGCT
TGTCAAAATCTCAACCGGAATGGGAAAGTTGCTGAATGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTTATCATTGTAAAAGATGGTGAATTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCCATAAAACTTATAAGTGATAAAAGAGTGGAAAGAGTATTGAGCCCGTTCATCATG
GTTTGGTCCCAGGTTCTGTTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTTATTGAAAGACCTGGATTGCCAGTGTGGGATCATATACT
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGA
AGATTGCTTGTCCCTCAAAAAGGCCAGACACCACAGCCATACCCATACCCTTCAAAAAAAT
TATTATCAGAAATCTGCACAAACCTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTCAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC
CATAAGACAACGCTCTGGTCCATCATTGCCACAGATAAATCTAGTTAAATTTTTATAG
TTATCTTAATATTATGATTTGATAAAACAGAAGATTGATCATTGTTGGTTGAAGTG
AACTGTGACTTTTGAAATTGCAAGGTTCACTCTAGATTGTCAATTAAATTGAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTATACAAGTTGAAATATGATTTAACAGTATGATG
GTTTAAATAGTTCTAATTGAAAAATCGTGCCAAGCAATAAGATTATGATATTGT
TTAATAATAAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAGTATTGCATTAT
TGAGGTATTAAAGAAGATTATTTAGAGAAAAATATTCTCATTTGATATAATTTTCTCTG
TTCACTGTGTGAAAAAAGAAGATATTTCCATAAATGGGAAGTTGCCATTGTCTCAAG
AAATGTTATTCAGTGACAATTCTGGTCTTTAGAGGTATATTCCAAATTCTCTGT
ATTTTAGGTTATGCAACTAATAAAACACTACCTTACATTAATTAAATTACAGTTCTACACA
TGGTAATACAGGATATGCTACTGATTAGGAAGTTTAAGTTCATGGTATTCTCTGATTC
CAACAAAGTTGATTCTCTGTATTCTACTTACTATGGTTACATTTTTATT
CAAATTGGATGATAATTCTGGAAACATTTTTATGTTTAGAAACAGTATT
GTTCAAACATGAAGTTACTGAGAGATCCATCAAATTGAACAACTGTTGAATTAAAATT
TTGCCACTTTTCAGATTACATCATTCTGCTGAACTTCAACTGAAATTGTTTTT
TTCTTTGGATGTGAAGGTGAACATTCTGATTGCTGTGATGTGAAAAAGCCTGGTA
TTTACATTGAAATTCAAAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAAG
CATCTTCTTGATATGCTAAATGTATTGTCCTCATATAACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTGATGTTAAAATAAAACATTTTTATATTGTTAAAAGACAA
ACTTCATATTCTGTGTTCTCCTGACTGGTAATATTGTGGGGATTTCACAGGTAAA
GTCAGTAGGATGGAACATTAGTGTATTCTAAAGAGCTAGAATACATAGTTT
CACCTTAAAGAAGGGGAAATCATAAAATACAATGAATCAACTGACCATTACGTAGTAGAC
AATTTCGTAAATGTCCCCCTTCTTAGGCTCTGTTGCTGTGAATCCATTAGATTACAG
TATCGTAATATACAAGTTCTTAAAGCCCTCTCCTTAGAATTAAAATATTGTACCATT
AAAGAGTTGGATGTGTAACTGTGATGCCTTAGAAAAATATCCTAACGACAAAATAAACCT
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIIFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLGLCMIFVADCLCPSKRRRPQPYPPSKKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCAGTGTCCAGCTCGGGAGACCGTGATAATTGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG
AAGTCCTGGCCCAGAGCAGTGACACTTCCCTGTGACCATGAAACTCTGGGTGTCTGC
ATTGCTGATGGCTGGTTGGTCTGAGCTGTGAGCTGTGAGGCGAATTCTCACCTCTATTG
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG
TGAAGCGGCTAACACACAGACTGGCCTGCGCTGGAGGACCTTGTGAGGACTCAGCTGCA
GGTTTATGCCAACCTCTGTGAGCGGCAGTTCTCCCCACTGATGAGGAGGAGATAGG
AGCTGCCAACGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGAACTTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG
GGCCGCTCGGCCTACAATGAAGGGACTATTATCATAACGGTGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGTGATGCCGGGGAGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGCTTCCAGTGGGTGATCTGACCGTGCCCTGGAGGCTCACCCGCCGCTGCTC
TCCCTGACCCAAAGCCACGAACGAGCTGGAGGAAATCTGCGGTACTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAAACGTTAACAAATCAGACAGAACGACTGAGCTAGCAACCCAGAAGGCA
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTCTGCGTGGG
GAGGGTGTCAAACGTACGACACCCGTAGACAGAACAGAGGCTTCTGTAGGTACCAACATGGCAA
CAGGGCCCCACAGCTGCTATTGCCCTTCAAAGAGGAGGACGGAGTGGACAGCCCGCACA
TCGTCAGGTACTACGATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
CCTAAACTTGCACGAGCCACCGTGTGATCCAAGACAGGAGCCTCACTGTCGCCAGCTA
CCGGGTTTCAAAAGCTCCTGGCTAGAGGAAGATGATGACCCCTGTTGGCCCGAGTAAATC
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT
TATGGAGTGGGAGGACAGTATGAACCGCACTCGACTTCTCTAGGCACCTTTGACAGCGG
CCTCAAAACAGAGGGAAATAGGTTAGGCACGTTCTTAACATGAGTGATGAGCTG
GTGGTGCCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTGCGGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCC
TGTGCTTGTGGCTGCAAGTGGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCCTTCTGTGCTTCCCTCCTGGTC
CTTCAGCCCATGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTGTCGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
GTGACTGAAGTCCCAGCCCTCCATTGAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
AAGTGGCTGAGCAGAGTTAGCTGTAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCAGTGAACCAAAGTTCTGATACCTGTTACATGTTGTTTAT
GGCATTCTATCTATTGTGGCTTACCAAAAAAATGCCCCACAGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGEELPGTKYQAMLSVDDCFGMGRSAYNEGDDYYHTV
LWMEQVLKQLDAGEEATTKSQVLDYLSYAVFQLGDLHRAELTRRLSLDPSHERAGGNLR
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVYDYLPERDVYESLCRGEGVKLTPRRQKRLF
CRYHGNRAPQLLIAPFKEEDEWDSPHIVRYDVMMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHDFDS
RRPFDGSLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEDYR
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTCCTCCTTTAGTGGAAAGACAGACATAATCCCAGTGTGAGTGAAATTGATTGT
TTCATTTATTACCGTTGGCTGGGGTTAGTTCCGACACCTTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGACAATCTTCTGGGGATGCTGGTCTGGAAAGCCAGCGGGCCTTGCCTGTCTTGGCCTCATTGACCC
CAGGTCTCTGGTAAACACTGAAAGCCTACTACTGGCCTGGTCCCCATCAATCCATTGATCCTTGAGGCTGTGCC
CCTGGGGCACCCACCTGGCAGGGCTACCAACCATGCACTGAGCTCCCTGTTGGCTCTGCTGCGGCCAGCGCTTC
CCCTCATCTTAGGGCTGCTCTGGGGTGCAGCCTGAGCCTCTGCGGGTTCTGGATCCAGGGGAGGGAGAAG
ATCCCTGTGTGAGGCTGTAGGGGAGCGAGGAGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG
ATGAAGACTTCAAACCCCGATTGCCCCACTACAGGGACCCACAAGCCTACAAGAAGGTGTCAGGACTC
GGTACATCCAGACAGAGCTGGCTCCGTGAGCGGTTGCTGGTGGCTGACCTCCGAGCTACACTGTCCA
CTTTGGCCGTGGCTGTGAACCGTACGGTGGCCCACATCACTTCCCTCGGTTACTCTACTTCACTGGCAGCGGGGG
CCCAGGCTCCAGCAGGGATGCAAGTGGTGTCTCATGGGATGAGCGGCCGCTGGCTCATGTCAGAGACCCCTGC
GCCACCTTCACACACACTTGGGGCCGACTACGACTGGTCTTCATCATGCAAGGATGACACATATGTGCAAGGCC
CCCGCCTGGCAGCCCTTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGCAGAGGAGTTCATTG
GCGCAGGCAGCAGGGCCCGTACTGTCACTGGGGCTTTGGCTACCTGTTGTCACGGAGTCTCCTGCTTCGTC
GCCACATCTGGATGGCTGCCAGGAGACATTCTCAGTGGCTCTGACGAGTGGCTTGGACGCTGCTCATTG
ACTCTCTGGGGCTGGCTGTGTCACAGCACAGGGCAGCAGTATGCTCATTTGAACACTGGCAAAATAGGG
ACCTGAGAAGCAAGGGAGCTGGCTTCTGAGTCCTGGCTGACCTGTCTCCGAAGGTACCCCTCATGT
ACCGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGCTTACAGTGAATAGAACAACTGCAAGGCTCAGA
TCCGAAACCTGACCGTGTGACCCCCGAAGGGGAGGCAAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCCTTCA
CACACACACTTCGCTTGGAGGTGCTGGCTGGACTACTTCACAGAGCAGCACACCTCTCTGTCAGATGGG
CTCCAAGTGCCTACTACAGGGGCTAGCAGGGCGACGGTGGTGTGCTGGAGACTGCCCTGAGCAGCTCA
ATCGCGCTATCAGCCCCGCTGCGCTTCCAGAAGCAGCGACTGCTCAACGGCTATCGCGCTTCCGACCCAGCAC
GGGCATGGAGTACACCCCTGGACCTGCTGGAAATCTACCTATGCCCTATGTCACTGAGGCCACCGAGTGC
GGTCAGCCTGCTGCCACTGAGCCGGTGGAAATCTACCTATGTCACTGAGGCCACCGAGTGC
AGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGAGCCCCGGCTTCTGAGGGCTTGAGCCAATGTCC
TGGAGCCAGAGAACATGCTCACCCTGTTGCTGGTCTACGGGCCACGAGAAGGTGGCCGGAGCTCCAG
ACCCATTCTGGGTGAAGGCTGAGCAGGGAGTTAGAGCAGGGTACCCCTGGACGAGGCTGGCTGGCTCG
CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGGACGTGGTCTGAAGAAGCACCCTGTGGACACTCTCT
TCTTCTTACCAACCGTGTGGACAAGGCTGGCCGAAGTCTCAACCGCTGCGCATGAATGCCATCTGCT
GGCAGGCCCTTCCAGTCCATTCCAGGAGTTCAATCCCTGCCCTGTCACCACAGAGATCACCCCCAGGGCCCC
CGGGGCTGGCCCTGACCCCCCTCCCTGGTGTGACCCCTCCGGGGCTCCTATAGGGGGAGATTG
ACCGGCAGGCTCTGCGAGGGCTGCTTCTACAACGCTGACTACCTGGCCGGCAGGCCGGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGCTGGAGGTGATGGATGTTCTCCGGTTCTCAGGGCTCC
ACCTTCTGGGGCGTAGAGGCCAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAGCCCACGGCTCAGTGAAG
AACTTACCAACCGCTGCCCTCAGCAACCTGGAGGGTAGGGGCCGTGCCAGCTGGCTATGGCTCTTTG
AGCAGGAGCAGCCAATAGCACTTAGCCCTGGGGCCCTAACCTTACCTTGTCTGCCAGCC
CCAGGAAGGGCAAGGAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTAAATATGAAAATGTTATTAA
ACATGTCTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEGEDPCVEAVGERGGPQNPDSRARLD
QSDEDFKPRIVPYYRDPNKPYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLRLRPHLDGCRG
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLPEGEAGLSWPVGLPAPFTPNSRFEV
LGWDYFTEQHTFSCADGAPKCPLOQASRADVGDALETALEQLNRRYQPRLRFQKQRLNGYR
RFDPARGMEYTL DLL ECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVPL
VAEAAAAPAFLEAFAAVLEPREHALLTLLL VYGPREGGRGAPDPFLGVKAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTWTRPGPEVLRCRMNAISGWQAFFP
VHFQEFNPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEALEGLEVMVDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRQLAMALFEQEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCACCGTGGAAACGTGAGAGGAAACCGTGCACCGCTGCCTTCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTGG
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTCATGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGCTGCAGTAAAGGAGACTGGACAAACACTGTGACAAAGCAG
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCAATTATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACAAC
GTTCTCCTGCACGCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTGAAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTAACAGCCTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTAATACAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC
CAACCAGGTAGTAGAAGGCTGTTCTGAGATATGGCTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGTGATGGGTATACCGCCTAGGGCATTGGCATATTTCAT
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTGTTGTCATTATTGTAGTAGTAACATATCCAA
TACAGCTGTATGTTCTTTCTTAATTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGGGTTTTCTTAAAACACATGAACATTGAAATG
TGTTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAACTATTAAATAATTATAT
GTGATAAAATTCTAAATTATGAAACATTAGAAATCTGTGGGGCACATATTGCTGATTGGTT
AAAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAACTTTAGCTGTGTTCCCTTACTTCTAATACTGATTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTGCTTCTCAAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAGTGAAGAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSENVKFESINMDTNMDWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDATMRDSS
NPRQNWNNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCGCCCGCTGCCGCTGGCCCTCAGCAACCCCTGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCTGCTGCTGCTTTCAGGGCTGCCTGATAGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCCCAGTGGTACAGGAATTGAAAGTGTGGAACTGTCTTGCATCATTACGGATTGCG
AGACAAGTGACCCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGCTGAGAAATACTGGGAAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTCAGGATGAAATGACCGAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGAACCCCTGTCTGAGAGTGGCAAGGCTGTACCAAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCAACTGCCACGGATT
CCAGAGCCAATCCAGATTGCAATTCTTCTTCACTTAAACTCTGAAACAGGCACTTGGTGTCACTGCTG
TTCACAAGGACGACTCTGGCAGTACTACTGCAATTGCTTCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGAATTATTGGGGGGTTCTGGTGTGCTTGTACTGGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGGCTACTTCATCAACAATAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACCAAGATGGAGTTAACTACATCCGCACTGACGAGGGCCACTTCAGACACAAGTCATGTTG
TGATCTGAGACCCGGGTGAGAGCGCACAGAGCGCACGTGACATACCTCTGCTAGAAACTCCTGTC
GGCAGCGAGAGCTGATGCACTGGCACAGAGCTAGAACACTCATTCAAGAGCTTGGCCAAAGTTGACCA
CTACTCTTCTTACTCTAACAGCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAAATATAACCAAA
GGAAGCGAAACTGGGTGGCTACTGAGTTGGCTTCAATCTGTTCTGGCTGATTCCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTGCTCACGTAACGCCCCTGCTGGCCCTGTGAAGCAGCATGTTACCAACTGGTC
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCGGGGAAACCA
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATGGCCACAGACACCACCGCAGTTCTTAAAGGCTCTG
TGATCGGTGTTGCACTGTTCAATTGGAGAAGCTTTGGATCAGCATTTGTTAAAACACCAAAATCAGGAAG
GTAAATTGGTTGCTGAAAGAGGATCTTGCCTGAGGAACCTGCTGTCACAGGGTGTCAAGGATTTAAGGAAA
ACCTCGTCTTAGGCTAACTGAAATGGTACTGAAATATGCTTCTATGGGCTTGTGTTATTAAACTG
TACATCTAAATTGGCTAAAGGATGTATTTGATTATTGAAAAGAAAATTCTATTTAAACTGTAATATATTGT
CATACAATGTTAAATAACCTATTTTAAAGGCTAACCTAACGGTAGAAGTCCAAGCTACTAGTGTAAAT
TGGAAAATATCAATAATTAGAGTATTTACCCAAGGAATCCTCTCATGGAAGTTACTGTGATGTTCTTCT
CACACAAGTTTAGCCTTTTCAAAAGGAACCTACACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAATTCCAGTTAACGAAATGTTGAAATCAGTTGCATCTCTTCAAAAGAACCTCTCAGGTTAGCTTGA
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAACGCTCAGATGTACATACAGATG
CCAGTCAGCTCTGGGTGCGCCAGGCGCCCCGCTAGCTCACTGCTCGCTGCTGCCAGGAGGCC
GCCATCCTGGCCCTGGCAGTGGCTGTGCTCCAGTGAGCTTACTCACGTGCCCTTGCTCATCCAGCACAGC
TCTCAGGTGGCACTGCAGGGACACTGGTGTCTTCCATGAGCTCCAGCTTGGCTCTGTAACAGACCTCT
TTTGTTATGGATGGCTACAAAATAGGGCCCCAATGCTATTTTTTAAAGTTGTTAATTATTGTT
AAGATTGCTAAGGCAAAGGAATGCGAAATCAACTGTCAGTACAATAACATTAAAAGAAAATGGAT
CCCACGTGCTCTTGCACAGAGAAAGCACCCAGGCCACAGGCTCTGTCGATTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAAGGTGGAGCAGCCAGGTGAAAGGCTGGGGAGGAAAG
TGAAAAGCCTGAATCAAAGCAGTTCTAATTGACTTTAAATTTCATCCGCCGAGACACTGCTCC
TGTGGGGGACATTAGCAACATCACTCAGAACGCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCC
GCCGTGCTGGACTCAGGACTGAAGTGTGAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGCTGCC
GAATGGCTCTCAACTCACCTGCTTCAAGCTTCAAGGTGTTTATACTTGACAGCTTTTT
AATTGCATACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGGCGCAGGCCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTGCTGCATGGCATCTGGATGTTAGCATGCAAGTTC
CCTCCATCATTGCCACCTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCCTGGGATTACGCTCCAGCCTC
TCTTGGTTGTCAGTGATAGGGTAGCCTTATTGCCCCCTTCTTATACCCCTAAACCTTCTACACTAGTGC
TGGGAAACCAGGCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTGTTGATTTAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATTATAAAAGCTTCAAAAAACCCA

FIGURE 124

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLFLLLFRGCLIGAVNLKSSNRTPVVQEFESELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267